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<p>(21) International Application Number: PCT/US98/20120 (22) International Filing Date: 25 September 1998 (25.09.98) (30) Priority Data: 08/937,540 25 September 1997 (25.09.97) US (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application US 08/937,540 (CIP) Filed on 25 September 1997 (25.09.97) (71) Applicant (for all designated States except US): WASHING- TON STATE UNIVERSITY RESEARCH FOUNDATION [US/US]; N.E. 1615 Eastgate Boulevard, Pullman, WA 99164-1802 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): CROTEAU, Rodney, Bruce [US/US]; 1835 N.E. Valley Road, Pullman, WA 99163 (US). WISE, Mitchell, Lynn [US/US]; 425A N.W. North Street, Pullman, WA 99163 (US). KATAHIRA, Eva, Joy [US/US]; 1720 N.E. Wheatland Drive, Pullman, WA 99163 (US). SAVAGE, Thomas, Jefferson [US/NZ]; 16 Cranbrook Avenue, Christchurch 5 (NZ).</p>	<p>(74) Agent: McGURL, Barry, F.; Christensen, O'Connor, Johnson & Kindness PLLC, Suite 2800, 1420 Fifth Avenue, Seattle, WA 98101 (US). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published With international search report.</p>	
<p>(54) Title: MONOTERPENE SYNTHASES FROM COMMON SAGE (<i>SALVIA OFFICINALIS</i>) (57) Abstract cDNAs encoding (+)-bomyl diphosphate synthase, 1-8-cineole synthase and (+)-sabinene synthase from common sage (<i>Salvia officinalis</i>) have been isolated and sequenced, and the corresponding amino acid sequences have been determined. Replicable recombinant cloning vehicles, host cells and the recombinant methods of making or enhanced expression of the enzymes in plants in order to increase the production of monoterpenoids or their products are provided.</p>		

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Monoterpene Synthases From Common Sage (*Salvia officinalis*)

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Field of the Invention

5 The present invention relates to nucleic acid sequences which code for monoterpene synthases (cyclases) from common sage (*Salvia officinalis*), and to vectors containing the sequences, host cells containing the sequences and methods of producing recombinant monoterpene synthases and their mutants.

Background of the Invention

10 The cyclization of the universal precursor geranyl diphosphate (GPP) to form monocyclic and bicyclic monoterpenes is catalyzed by a group of enzymes termed monoterpene synthases (or cyclases). The biochemical transformation of GPP to cyclic products has been investigated using enzymes from a variety of plants, including both angiosperms (Croteau, R., *Chem. Rev.* 87:929-954, 1987) and
15 gymnosperms (Lewinsohn et al., *Arch. Biochem. Biophys.* 293:167-173, 1992; Savage et al., *J. Biol. Chem.* 269:4012-4020, 1994; Savage et al., *Arch. Biochem. Biophys.* 320:257-265, 1995). A mechanistic paradigm for these transformations is well established (Croteau, R., *Chem. Rev.* 87:929-954, 1987; Wise, M. L., and Croteau, R., in *Comprehensive Natural Products Chemistry: Isoprenoids*
20 (Cane, D.E., ed) Vol. 2 (in press), Elsevier Science, Oxford, 1998). In summary, geranyl diphosphate is initially ionized and isomerized to form either 3*R*- or 3*S*-linalyl diphosphate, depending on the particular enzyme, which is converted to the α -terpinyl cation as a central intermediate. Further transformations of this reactive intermediate may be effected by additional intramolecular electrophilic additions, hydride shifts or
25 other rearrangements before termination of the sequence by deprotonation of the final

cation or capture by an external nucleophile, such as a hydroxyl ion or the diphosphate group. Although the fate of the substrate has been well characterized in numerous monoterpene cyclization reactions, the molecular mechanisms by which the enzymes effect these transformations is still poorly understood.

5 Culinary sage (*Salvia officinalis*) produces a number of monoterpenes, including (+)- and (-)- α -pinene, (+)- and (-)- β -pinene, (+)- and (-)-camphene, (+)-sabinene, (+)- and (-)-limonene, myrcene, 1,8-cineole, and (+)-bornyl diphosphate (Croteau, R., *Chem. Rev.* 87:929-954, 1987). Because sage produces this broad
10 range of acyclic, monocyclic and bicyclic monoterpenes, including several olefin isomers, a cyclic ether and a diphosphate ester, this plant has provided an ideal system for the study of a variety of biosynthetic enzymes, all of which utilize the same substrate but produce different products by variations on a single reaction mechanism (Croteau, R., *Chem. Rev.* 87:929-954, 1987; Wise, M. L., and Croteau, R., in *Comprehensive Natural Products Chemistry: Isoprenoids* (Cane, D.E., ed) Vol. 2 (in
15 press), Elsevier Science, Oxford, 1998). These monoterpene synthases include (+)-bornyl diphosphate synthase (the enzyme producing the precursor of (+)-camphor) (Croteau, R., and Karp, F., *Arch. Biochem. Biophys.* 198:512-522, 1979; Croteau, R., and Karp, F., *Arch. Biochem. Biophys.* 198:523-532, 1979), 1,8-cineole synthase (Croteau et al, *Arch. Biochem. Biophys.* 309:184-192, 1994),
20 (+)-sabinene synthase (the enzyme producing the precursor of (-)-3-isothujone) (Croteau, R., in *Recent Developments in Flavor and Fragrance Chemistry* (Hopp, R., and Mori, K., eds), pp. 263-273, VCH, Weinheim, Germany, 1992; Croteau, R., in *Flavor Precursors: Thermal and Enzymatic Conversions* (Teranishi, R., Takeoka, G. R., and Guntert, M., eds), American Chemical Society Symposium Series, No. 490,
25 pp. 8-20, Washington, DC, 1992), and several pinene synthases (Gambliel, H., and Croteau, R., *J. Biol. Chem.* 257:2335-2342, 1982; Gambliel, H., and Croteau, R., *J. Biol. Chem.* 259:740-748, 1984; Wagschal et al., *Arch. Biochem. Biophys.* 308:477-487, 1994; Pyun et al., *Arch. Biochem. Biophys.* 308:488-496, 1994).

As is typical of monoterpene cyclases, many of these enzymes from sage
30 generate multiple products from geranyl diphosphate (Wise, M. L., and Croteau, R., in *Comprehensive Natural Products Chemistry: Isoprenoids* (Cane, D. E., ed) Vol. 2 (in press), Elsevier Science, Oxford, 1998; Wagschal et al., *Tetrahedron* 47:5933-5944, 1991). For example, investigations with the partially purified native enzymes have suggested that a single enzyme, termed (+)-pinene synthase (cyclase I),
35 is responsible for the synthesis of both (+)- α -pinene and (+)-camphene, with lesser

amounts of (+)-limonene and myrcene, whereas a second enzyme, (-)-pinene synthase (cyclase II), has been shown to produce (-)- α -pinene, (-)- β -pinene and (-)-camphene, with minor amounts of (-)-limonene, terpinolene and myrcene (Gambliel, H., and Croteau, R., *J. Biol. Chem.* **257**:2335-2342, 1982; Gambliel, H., and Croteau, R., *J. Biol. Chem.* **259**:740-748, 1984).

More recently, a third synthase from sage, termed cyclase III, has been described which produces a mixture of (+)- α -pinene and (+)- β -pinene, along with minor amounts of myrcene (Wagschal et al., *Arch. Biochem. Biophys.* **308**:477-487, 1994; Pyun et al., *Arch. Biochem. Biophys.* **308**:488-496, 1994). Evidence that these reactions are catalyzed by individual, multifunctional enzymes is provided by co-purification and differential inhibition studies (Gambliel, H., and Croteau, R., *J. Biol. Chem.* **259**:740-748, 1984), as well as by isotopically sensitive branching experiments (Wagschal et al., *Arch. Biochem. Biophys.* **308**:477-487, 1994; Wagschal et al., *Tetrahedron* **47**:5933-5944, 1991; Croteau et al., *Biochemistry* **26**:5383-5389, 1987). In spite of considerable effort, the (+)-pinene synthase has never been chromatographically separated from the aforementioned (+)-bornyl diphosphate synthase, suggesting that (+)-bornyl diphosphate synthase and (+)-pinene synthase might, in fact, be a single, multifunctional enzyme (McGeady, P., and Croteau, R., *Arch. Biochem. Biophys.* **317**:149-155, 1995). Similarly, the (-)-pinene synthase has never been fully resolved from 1,8-cineole synthase, although, in this case, stereochemical considerations indicate that the two are distinct enzyme species (Croteau et al., *Arch. Biochem. Biophys.* **309**:184-192, 1994; Croteau et al., *J. Biol. Chem.* **264**:2075-2080, 1989).

The unusual ability of the monoterpene synthases to synthesize multiple products from a single substrate requires the nomenclature of these enzymes to be based on the identity of the principal product synthesized by each enzyme. Thus, starting from the common precursor geranyl diphosphate, (+)-bornyl diphosphate synthase characteristically produces a mixture of monoterpenes of which at least 60% is (+)-bornyl diphosphate; 1,8-cineole synthase characteristically produces a mixture of monoterpenes of which at least 60% is 1,8-cineole and (+)-sabinene synthase characteristically produces a mixture of monoterpenes of which at least 60% is (+)-sabinene.

Summary of the Invention

In accordance with the foregoing, cDNAs encoding (+)-bornyl diphosphate synthase, 1,8-cineole synthase and (+)-sabinene synthase from common sage (*Salvia*

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officinalis) have been isolated and sequenced, and the corresponding amino acid sequences have been deduced. Accordingly, the present invention relates to isolated angiosperm DNA sequences which code for the expression of (+)-bornyl diphosphate synthase, such as the sequence designated SEQ ID No:1 which encodes (+)-bornyl diphosphate synthase from common sage (*Salvia officinalis*), for the expression of 1,8-cineole synthase, such as the sequence designated SEQ ID No:3, which encodes 1,8-cineole synthase from common sage (*Salvia officinalis*), and for the expression of (+)-sabinene synthase, such as the sequence designated SEQ ID No:5, which encodes the (+)-sabinene synthase from common sage (*Salvia officinalis*). In other aspects, the present invention is directed to replicable recombinant cloning vehicles comprising a nucleic acid sequence, e.g., a DNA sequence which codes for a (+)-bornyl diphosphate synthase, 1,8-cineole synthase or (+)-sabinene synthase, or for a base sequence sufficiently complementary to at least a portion of DNA or RNA encoding (+)-bornyl diphosphate synthase, 1,8-cineole synthase or (+)-sabinene synthase to enable hybridization therewith (e.g., antisense RNA or fragments of DNA complementary to a portion of DNA or RNA molecules encoding (+)-bornyl diphosphate synthase, 1,8-cineole synthase or (+)-sabinene synthase which are useful as polymerase chain reaction primers or as probes for any of the foregoing synthases or related genes). In yet other aspects of the invention, modified host cells are provided that have been transformed, transfected, infected and/or injected with a recombinant cloning vehicle and/or DNA sequence of the invention. Thus, the present invention provides for the recombinant expression of (+)-bornyl diphosphate synthase, 1,8-cineole synthase and (+)-sabinene synthase, and the inventive concepts may be used to facilitate the production, isolation and purification of significant quantities of recombinant (+)-bornyl diphosphate synthase, 1,8-cineole synthase and (+)-sabinene synthase (or of their primary enzyme products) for subsequent use, to obtain expression or enhanced expression of (+)-bornyl diphosphate synthase, 1,8-cineole synthase and (+)-sabinene synthase in plants, microorganisms or animals, or may be otherwise employed in an environment where the regulation or expression of (+)-bornyl diphosphate synthase, 1,8-cineole synthase and (+)-sabinene synthase is desired for the production of these synthases, or their enzyme products, or derivatives thereof.

Brief Description of the Drawings

The foregoing aspects and many of the attendant advantages of this invention will become more readily appreciated as the same becomes better understood by

reference to the following detailed description, when taken in conjunction with the accompanying drawings, wherein:

FIGURE 1 shows the terpenoid biosynthetic reactions catalyzed by (+)-bornyl diphosphate synthase (1), (+)-sabinene synthase (2) and 1,8-cineole synthase (3).

5

Detailed Description of the Preferred Embodiment

As used herein, the terms "amino acid" and "amino acids" refer to all naturally occurring L- α -amino acids or their residues. The amino acids are identified by either the single-letter or three-letter designations:

10	Asp	D	aspartic acid	Ile	I	isoleucine
	Thr	T	threonine	Leu	L	leucine
	Ser	S	serine	Tyr	Y	tyrosine
	Glu	E	glutamic acid	Phe	F	phenylalanine
15	Pro	P	proline	His	H	histidine
	Gly	G	glycine	Lys	K	lysine
	Ala	A	alanine	Arg	R	arginine
	Cys	C	cysteine	Trp	W	tryptophan
	Val	V	valine	Gln	Q	glutamine
	Met	M	methionine	Asn	N	asparagine

As used herein, the term "nucleotide" means a monomeric unit of DNA or RNA containing a sugar moiety (pentose), a phosphate and a nitrogenous heterocyclic base. The base is linked to the sugar moiety via the glycosidic carbon (1' carbon of pentose) and that combination of base and sugar is called a nucleoside. The base characterizes the nucleotide with the four bases of DNA being adenine ("A"), guanine ("G"), cytosine ("C") and thymine ("T"). Inosine ("I") is a synthetic base that can be used to substitute for any of the four, naturally-occurring bases (A, C, G or T). The four RNA bases are A, G, C and uracil ("U"). The nucleotide sequences described herein comprise a linear array of nucleotides connected by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

The term "angiosperm" refers to a group of plants that produce seeds that are enclosed within an ovary. An example of an angiosperm plant species is sage (*Salvia officinalis*).

The term "essential oil plant," or "essential oil plants," refers to a group of plant species that produce high levels of monoterpenoid and/or sesquiterpenoid and/or diterpenoid oils, and/or high levels of monoterpenoid and/or sesquiterpenoid and/or diterpenoid resins. The foregoing oils and/or resins account for greater than about

0.005% of the fresh weight of an essential oil plant that produces them. The essential oils and/or resins are more fully described, for example, in *E. Guenther, The Essential Oils, Vols. I-VI, R.E. Krieger Publishing Co., Huntington N.Y., 1975*, incorporated herein by reference. The essential oil plants include, but are not limited to:

5 Lamiaceae, including, but not limited to, the following species: Ocimum (basil), Lavandula (Lavender), Origanum (oregano), Mentha (mint), Salvia (sage), Rosmecinus (rosemary), Thymus (thyme), Satureja and Monarda.

 Umbelliferae, including, but not limited to, the following species: Carum (caraway), Anethum (dill), feniculum (fennel) and Daucus (carrot).

10 Asteraceae (Compositae), including, but not limited to, the following species: Artemisia (tarragon, sage brush), Tanacetum (tansy).

 Rutaceae (e.g., citrus plants); Rosaceae (e.g., roses); Myrtaceae (e.g., eucalyptus, Melaleuca); the Gramineae (e.g., Cymbopogon (citronella)); Geranaceae (Geranium) and certain conifers including Abies (e.g., Canadian balsam), Cedrus
15 (cedar) and Thuja and Juniperus.

 The range of essential oil plants is more fully set forth in *E. Guenther, The Essential Oils, Vols. I-VI, R.E. Krieger Publishing Co., Huntington N.Y., 1975*, which is incorporated herein by reference.

20 The term "percent identity" means the percentage of amino acids or nucleotides that occupy the same relative position when two amino acid sequences, or two nucleic acid sequences are aligned side by side.

 The term "percent similarity" is a statistical measure of the degree of relatedness of two compared protein sequences. The percent similarity is calculated by a computer program that assigns a numerical value to each compared pair of amino
25 acids based on chemical similarity (e.g., whether the compared amino acids are acidic, basic, hydrophobic, aromatic, etc.) and/or evolutionary distance as measured by the minimum number of base pair changes that would be required to convert a codon encoding one member of a pair of compared amino acids to a codon encoding the other member of the pair. Calculations are made after a best fit alignment of the two
30 sequences have been made empirically by iterative comparison of all possible alignments. (Henikoff, S. and Henikoff, J.G., *Proc. Nat'l Acad Sci USA* 89:10915-10919, 1992).

 "Oligonucleotide" refers to short length single or double stranded sequences of deoxyribonucleotides linked via phosphodiester bonds. The oligonucleotides are

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chemically synthesized by known methods and purified, for example, on polyacrylamide gels.

The term "(+)-bornyl diphosphate synthase" is used herein to mean an enzyme capable of generating multiple monoterpenes from geranyl diphosphate. The principal and characteristic monoterpene synthesized by (+)-bornyl diphosphate synthase is bornyl pyrophosphate, which comprises at least 60% of the monoterpene mixture synthesized by (+)-bornyl diphosphate synthase from geranyl diphosphate.

The term "(+)-sabinene synthase" is used herein to mean an enzyme capable of generating multiple monoterpenes from geranyl diphosphate. The principal and characteristic monoterpene synthesized by (+)-sabinene synthase is sabinene, which comprises at least 60% of the monoterpene mixture synthesized by (+)-sabinene synthase from geranyl diphosphate.

The term "1,8-cineole synthase" is used herein to mean an enzyme capable of generating multiple monoterpenes from geranyl diphosphate. The principal and characteristic monoterpene synthesized by 1,8-cineole synthase is 1,8 cineole, which comprises at least 60% of the monoterpene mixture synthesized by 1,8-cineole synthase from geranyl diphosphate.

The terms "alteration", "amino acid sequence alteration", "variant" and "amino acid sequence variant" refer to (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase molecules with some differences in their amino acid sequences as compared to the corresponding, native, *i.e.*, naturally-occurring, synthases. Ordinarily, the variants will possess at least about 70% homology with the corresponding native synthases, and preferably, they will be at least about 80% homologous with the corresponding, native synthases. The amino acid sequence variants of (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase falling within this invention possess substitutions, deletions, and/or insertions at certain positions. Sequence variants of (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase may be used to attain desired enhanced or reduced enzymatic activity, modified regiochemistry or stereochemistry, or altered substrate utilization or product distribution.

Substitutional (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase variants are those that have at least one amino acid residue in the native synthase sequence removed and a different amino acid inserted in its place at the same position. The substitutions may be single, where only one amino acid in the molecule has been substituted, or they may be multiple, where two or more amino

acids have been substituted in the same molecule. Substantial changes in the activity of the (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase molecules may be obtained by substituting an amino acid with a side chain that is significantly different in charge and/or structure from that of the native amino acid. This type of substitution would be expected to affect the structure of the polypeptide backbone and/or the charge or hydrophobicity of the molecule in the area of the substitution.

Moderate changes in the activity of the (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase molecules would be expected by substituting an amino acid with a side chain that is similar in charge and/or structure to that of the native molecule. This type of substitution, referred to as a conservative substitution, would not be expected to substantially alter either the structure of the polypeptide backbone or the charge or hydrophobicity of the molecule in the area of the substitution.

Insertional (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase variants are those with one or more amino acids inserted immediately adjacent to an amino acid at a particular position in the native synthase molecule. Immediately adjacent to an amino acid means connected to either the α -carboxy or α -amino functional group of the amino acid. The insertion may be one or more amino acids. Ordinarily, the insertion will consist of one or two conservative amino acids. Amino acids similar in charge and/or structure to the amino acids adjacent to the site of insertion are defined as conservative. Alternatively, this invention includes insertion of an amino acid with a charge and/or structure that is substantially different from the amino acids adjacent to the site of insertion.

Deletional variants are those where one or more amino acids in the native (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase molecules have been removed. Ordinarily, deletional variants will have one or two amino acids deleted in a particular region of the (+)-bornyl diphosphate synthase, (+)-sabinene synthase or 1,8-cineole synthase molecule.

The terms "biological activity", "biologically active", "activity" and "active" refer to the ability of (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase molecules to convert geranyl diphosphate to a group of monoterpenes, of which bornyl pyrophosphate is the principal and characteristic monoterpene synthesized by (+)-bornyl diphosphate synthase, sabinene is the principal and characteristic monoterpene synthesized by (+)-sabinene synthase and 1,8-cineole

is the principal and characteristic monoterpene synthesized by 1,8-cineole synthase. The monoterpenes produced by (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase are as measured in an enzyme activity assay, such as the assay described in Example 3. Amino acid sequence variants of (+)-bornyl
5 diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase may have desirable altered biological activity including, for example, altered reaction kinetics, substrate utilization product distribution or other characteristics such as regiochemistry and stereochemistry.

The terms "DNA sequence encoding", "DNA encoding" and "nucleic acid
10 encoding" refer to the order or sequence of deoxyribonucleotides along a strand of deoxyribonucleic acid. The order of these deoxyribonucleotides determines the order of amino acids along the translated polypeptide chain. The DNA sequence thus codes for the amino acid sequence.

The terms "replicable expression vector" and "expression vector" refer to a
15 piece of DNA, usually double-stranded, which may have inserted into it a piece of foreign DNA. Foreign DNA is defined as heterologous DNA, which is DNA not naturally found in the host. The vector is used to transport the foreign or heterologous DNA into a suitable host cell. Once in the host cell, the vector can replicate independently of or coincidental with the host chromosomal DNA, and
20 several copies of the vector and its inserted (foreign) DNA may be generated. In addition, the vector contains the necessary elements that permit translating the foreign DNA into a polypeptide. Many molecules of the polypeptide encoded by the foreign DNA can thus be rapidly synthesized.

The terms "transformed host cell," "transformed" and "transformation" refer to
25 the introduction of DNA into a cell. The cell is termed a "host cell", and it may be a prokaryotic or a eukaryotic cell. Typical prokaryotic host cells include various strains of *E. coli*. Typical eukaryotic host cells are plant cells, such as maize cells, yeast cells, insect cells or animal cells. The introduced DNA is usually in the form of a vector containing an inserted piece of DNA. The introduced DNA sequence may be
30 from the same species as the host cell or from a different species from the host cell, or it may be a hybrid DNA sequence, containing some foreign DNA and some DNA derived from the host species.

The abbreviation "SSC" refers to a buffer used in nucleic acid hybridization solutions. One liter of the 20X (twenty times concentrate) stock SSC buffer solution
35 (pH 7.0) contains 175.3 g sodium chloride and 88.2 g sodium citrate.

The following abbreviations are used herein: bp(s), base pair(s); DEAE, *O*-diethylaminoethyl; DTT, dithiothreitol; EDTA, ethylenediaminetetraacetic acid; GC, gas chromatography; IPTG, isopropyl- β -D-thiogalactopyranoside; LB, Luria-Bertani; Mopso, 3-(*N*-morpholino)-2-hydroxypropane-sulfonic acid; MS, mass spectrum/spectrometry; nt(s), nucleotide(s); ORF, open reading frame; PCR, polymerase chain reaction; PVDF, polyvinylidenedifluoride; SDS, sodium dodecyl sulfate; SBS, sage bornyl diphosphate synthase; SCS, sage 1,8-cineole synthase; SSS, sage sabinene synthase; Tris, tris(hydroxymethyl) aminomethane; UV, ultraviolet.

In accordance with the present invention, cDNAs encoding (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase were isolated and sequenced in the following manner. An homology-based PCR strategy was utilized that is a modified version of a published, homology-based PCR strategy (Steele et al., *Proc. Natl. Acad. Sci. USA* 92:4164-4168, 1995). A comparison was made of the deduced amino acid sequences of cDNAs encoding mechanistically-related, but phylogenetically diverse, enzymes involved in terpenoid biosynthesis (Colby et al., *J. Biol. Chem.* 268:23016-23024, 1993; Yuba et al., *Arch. Biochem. Biophys.* 332:280-287, 1996; Bohlmann et al., *J. Biol. Chem.* 272:21784-21792, 1997). Three conserved regions of sequence were identified that appeared to be useful for the design of degenerate PCR primers. Two of these primers ultimately amplified a 600 bp fragment using cDNA from a phagemid sage leaf library as target. Cloning and sequencing showed that the amplified 600 bp product comprised two distinct sequence groups, both of which showed similarity to sequences of cloned terpene synthases, but only one of which hybridized strongly to a 2 kb target upon northern blot analysis of sage leaf mRNA. This more efficient probe was utilized to screen the sage leaf cDNA library, from which 77 positive phagemids were purified. Size selection of the purified and *in vivo* excised clones yielded a subset of 44 with inserts >1.6 kb, and these were expressed in *E. coli* XL1-Blue and assayed for functional monoterpene synthase activity by monitoring the conversion of [1-³H]geranyl diphosphate to monoterpene olefins, oxygenated monoterpenes and monoterpenyl diphosphate esters.

Two cDNA clones, of which the clone designated 3C6 was more active in expression, yielded an enzyme in the corresponding bacterial extracts that produced principally bornyl diphosphate from geranyl diphosphate. This recombinant enzyme, designated SBS (sage bornyl diphosphate synthase), was presumed to represent the native (+)-bornyl diphosphate synthase of sage, one of the prominent enzymes of oil

gland extracts (Croteau, R., and Karp, F., *Arch. Biochem. Biophys.* **198**:512-522, 1979) that produces the first dedicated intermediate in (+)-camphor biosynthesis (Croteau, R., and Karp, F., *Arch. Biochem. Biophys.* **198**:523-532, 1979; Croteau, R., and Karp, F., *Arch. Biochem. Biophys.* **184**:77-86, 1977; Croteau et al., *Arch. Biochem. Biophys.* **188**:182-193, 1978).

Four cDNA clones, of which clone 3B5 was apparently most active, expressed a synthase in bacterial extracts that converted geranyl diphosphate to 1,8-cineole as the major product. This acquisition was designated SCS (sage 1,8-cineole synthase) and considered to represent the native 1,8-cineole synthase, an enzyme for which the mechanism of cyclization has been studied in detail (Croteau et al., *Arch. Biochem. Biophys.* **309**:184-192, 1994; Croteau, R., and Karp, F., *Arch. Biochem. Biophys.* **179**:257-265, 1977).

Two additional clones, of which clone 3F25 was the more active in expression, yielded *E. coli* extracts capable of transforming geranyl diphosphate to sabinene as the dominant olefin product. This acquisition was named SSS (sage sabinene synthase), with correspondence assigned to the native (+)-sabinene synthase that catalyzes the cyclization to the bicyclic olefin precursor of (-)-isothujone (Croteau, R. in *Recent Developments in Flavor and Fragrance Chemistry* (Hopp, R., and Mori, K., eds), pp. 263-273, VCH, Weinheim, Germany, 1992; Croteau, R., in *Flavor Precursors: Thermal and Enzymatic Conversions* (Teranishi, R., Takeoka, G.R., and Guntert, M., eds), American Chemical Society Symposium Series, No. 490, pp. 8-20, Washington, DC, 1992; Karp, F., and Croteau, R., *Arch. Biochem. Biophys.* **216**:616-624, 1982).

From the DNA sequence of Clones 3C6 (SEQ ID No:1), 3B5 (SEQ ID No:3) and 3F25 (SEQ ID No:5) the corresponding amino acid sequences of (+)-bornyl diphosphate synthase (SBS) (SEQ ID No:2), 1,8-cineole synthase (SCS) (SEQ ID No:4) and (+)-sabinene synthase (SSS) (SEQ ID No:6), respectively, were deduced.

Additionally, sequencing of cDNA clones that hybridized to the 600bp prenyltransferase probe, but which did not express detectable monoterpene cyclase activity in bacterial extracts, revealed an additional clone, designated 3F5 (SEQ ID No:7). The DNA sequence of clone 3F5 is similar to the sequences of clones 3C6, 3B5 and 3F25, and appears to represent a novel monoterpene cyclase clone. Clone 3F5 contains a premature, translational stop codon, consequently clone 3F5 does not encode a functional monoterpene cyclase.

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The isolation of cDNAs encoding (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase permits the development of efficient expression systems for these functional enzymes; provides useful tools for examining the developmental regulation of monoterpene biosynthesis; permits investigation of the reaction mechanism(s) of these unusual, multiproduct enzymes, and permits the isolation of other (+)-bornyl diphosphate synthases, (+)-sabinene synthases and 1,8-cineole synthases. The isolation of the (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase cDNAs also permits the transformation of a wide range of organisms in order to introduce monoterpene biosynthesis *de novo*, or to modify endogenous monoterpene biosynthesis.

Although the (+)-bornyl diphosphate synthase, 1,8-cineole synthase and (+)-sabinene synthase proteins set forth in SEQ ID Nos:2, 4 and 6, respectively, direct the enzymes to plastids, substitution of the targeting sequence of each of these enzymes (SEQ ID No:2, amino acids 1 to 56; SEQ ID No:4, amino acids 1 to 58; SEQ ID No:6, amino acids 1 to 53) with other transport sequences well known in the art (see, e.g., von Heijne et al., *Eur. J. Biochem.* **180**:535-545, 1989; Stryer, *Biochemistry*, W.H. Freeman and Company, New York, NY, p. 769 [1988]) may be employed to direct the (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase to other cellular or extracellular locations.

In addition to the native (+)-bornyl diphosphate synthase, 1,8-cineole synthase and (+)-sabinene synthase amino acid sequences of SEQ ID No:2, SEQ ID No:4 and SEQ ID No:6, respectively, sequence variants produced by deletions, substitutions, mutations and/or insertions are intended to be within the scope of the invention except insofar as limited by the prior art. The (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase amino acid sequence variants of this invention may be constructed by mutating the DNA sequences that encode the wild-type synthases, such as by using techniques commonly referred to as site-directed mutagenesis. Various polymerase chain reaction (PCR) methods, now well known in the field, such as a two primer system like the Transformer Site-Directed Mutagenesis kit from Clontech, may be employed for this purpose.

Following denaturation of the target plasmid in this system, two primers are simultaneously annealed to the plasmid; one of these primers contains the desired site-directed mutation, the other contains a mutation at another point in the plasmid resulting in elimination of a restriction site. Second strand synthesis is then carried out, tightly linking these two mutations, and the resulting plasmids are transformed

into a *mutS* strain of *E. coli*. Plasmid DNA is isolated from the transformed bacteria, restricted with the relevant restriction enzyme (thereby linearizing the unmutated plasmids), and then retransformed into *E. coli*. This system allows for generation of mutations directly in an expression plasmid, without the necessity of subcloning or generation of single-stranded phagemids. The tight linkage of the two mutations and the subsequent linearization of unmutated plasmids results in high mutation efficiency and allows minimal screening. Following synthesis of the initial restriction site primer, this method requires the use of only one new primer type per mutation site. Rather than prepare each positional mutant separately, a set of "designed degenerate" oligonucleotide primers can be synthesized in order to introduce all of the desired mutations at a given site simultaneously. Transformants can be screened by sequencing the plasmid DNA through the mutagenized region to identify and sort mutant clones. Each mutant DNA can then be restricted and analyzed by electrophoresis on Mutation Detection Enhancement gel (J.T. Baker) to confirm that no other alterations in the sequence have occurred (by band shift comparison to the unmutagenized control).

The verified mutant duplexes in the pET (or other) overexpression vector can be employed to transform *E. coli* such as strain *E. coli* BL21(DE3)pLysS, for high level production of the mutant protein, and purification by standard protocols. The method of FAB-MS mapping can be employed to rapidly check the fidelity of mutant expression. This technique provides for sequencing segments throughout the whole protein and provides the necessary confidence in the sequence assignment. In a mapping experiment of this type, protein is digested with a protease (the choice will depend on the specific region to be modified since this segment is of prime interest and the remaining map should be identical to the map of unmutagenized protein). The set of cleavage fragments is fractionated by microbore HPLC (reversed phase or ion exchange, again depending on the specific region to be modified) to provide several peptides in each fraction, and the molecular weights of the peptides are determined by FAB-MS. The masses are then compared to the molecular weights of peptides expected from the digestion of the predicted sequence, and the correctness of the sequence quickly ascertained. Since this mutagenesis approach to protein modification is directed, sequencing of the altered peptide should not be necessary if the MS agrees with prediction. If necessary to verify a changed residue, CAD-tandem MS/MS can be employed to sequence the peptides of the mixture in question, or the

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target peptide purified for subtractive Edman degradation or carboxypeptidase Y digestion depending on the location of the modification.

In the design of a particular site directed mutagenesis, it is generally desirable to first make a non-conservative substitution (e.g., Ala for Cys, His or Glu) and determine if activity is greatly impaired as a consequence. The properties of the mutagenized protein are then examined with particular attention to the kinetic parameters of K_m and k_{cat} as sensitive indicators of altered function, from which changes in binding and/or catalysis *per se* may be deduced by comparison to the native enzyme. If the residue is by this means demonstrated to be important by activity impairment, or knockout, then conservative substitutions can be made, such as Asp for Glu to alter side chain length, Ser for Cys, or Arg for His. For hydrophobic segments, it is largely size that is usefully altered, although aromatics can also be substituted for alkyl side chains. Changes in the normal product distribution can indicate which step(s) of the reaction sequence have been altered by the mutation. Modification of the hydrophobic pocket can be employed to change binding conformations for substrates and result in altered regiochemistry and/or stereochemistry.

Other site directed mutagenesis techniques may also be employed with the nucleotide sequences of the invention. For example, restriction endonuclease digestion of DNA followed by ligation may be used to generate deletion variants of (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase, as described in section 15.3 of Sambrook et al. (*Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press, New York, NY [1989]). A similar strategy may be used to construct insertion variants, as described in section 15.3 of Sambrook et al., *supra*.

Oligonucleotide-directed mutagenesis may also be employed for preparing substitution variants of this invention. It may also be used to conveniently prepare the deletion and insertion variants of this invention. This technique is well known in the art as described by Adelman et al. (*DNA* 2:183 [1983]). Generally, oligonucleotides of at least 25 nucleotides in length are used to insert, delete or substitute two or more nucleotides in the (+)-bornyl diphosphate synthase, (+)-sabinene synthase or 1,8-cineole synthase molecule. An optimal oligonucleotide will have 12 to 15 perfectly matched nucleotides on either side of the nucleotides coding for the mutation. To mutagenize wild-type (+)-bornyl diphosphate synthase, (+)-sabinene synthase or 1,8-cineole synthase, the oligonucleotide is annealed to the single-stranded DNA template

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molecule under suitable hybridization conditions. A DNA polymerizing enzyme, usually the Klenow fragment of *E. coli* DNA polymerase I, is then added. This enzyme uses the oligonucleotide as a primer to complete the synthesis of the mutation-bearing strand of DNA. Thus, a heteroduplex molecule is formed such that
5 one strand of DNA encodes the wild-type synthase inserted in the vector, and the second strand of DNA encodes the mutated form of the synthase inserted into the same vector. This heteroduplex molecule is then transformed into a suitable host cell.

Mutants with more than one amino acid substituted may be generated in one of several ways. If the amino acids are located close together in the polypeptide
10 chain, they may be mutated simultaneously using one oligonucleotide that codes for all of the desired amino acid substitutions. If however, the amino acids are located some distance from each other (separated by more than ten amino acids, for example) it is more difficult to generate a single oligonucleotide that encodes all of the desired changes. Instead, one of two alternative methods may be employed. In the first
15 method, a separate oligonucleotide is generated for each amino acid to be substituted. The oligonucleotides are then annealed to the single-stranded template DNA simultaneously, and the second strand of DNA that is synthesized from the template will encode all of the desired amino acid substitutions. An alternative method involves two or more rounds of mutagenesis to produce the desired mutant. The first
20 round is as described for the single mutants: wild-type (+)-bornyl diphosphate synthase, (+)-sabinene synthase or 1,8-cineole synthase DNA is used for the template, an oligonucleotide encoding the first desired amino acid substitution(s) is annealed to this template, and the heteroduplex DNA molecule is then generated. The second round of mutagenesis utilizes the mutated DNA produced in the first round of
25 mutagenesis as the template. Thus, this template already contains one or more mutations. The oligonucleotide encoding the additional desired amino acid substitution(s) is then annealed to this template, and the resulting strand of DNA now encodes mutations from both the first and second rounds of mutagenesis. This resultant DNA can be used as a template in a third round of mutagenesis, and so on.

30 A gene encoding (+)-bornyl diphosphate synthase, (+)-sabinene synthase or 1,8-cineole synthase may be incorporated into any organism (intact plant, animal, microbe, etc.), or cell culture derived therefrom, that produces geranyl diphosphate. A (+)-bornyl diphosphate synthase, (+)-sabinene synthase or 1,8-cineole synthase gene may be introduced into any organism for a variety of purposes including, but not
35 limited to: production of (+)-bornyl diphosphate synthase, (+)-sabinene synthase or

1,8-cineole synthase, or their products; production or modification of flavor and aroma properties; improvement of defense capability, and the alteration of other ecological interactions mediated by bornyl pyrophosphate, sabinene, 1,8-cineole, or their derivatives.

5 Eukaryotic expression systems may be utilized for the production of (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase since they are capable of carrying out any required posttranslational modifications and of directing the enzymes to the proper membrane location. A representative eukaryotic expression system for this purpose uses the recombinant baculovirus, *Autographa*
10 *californica* nuclear polyhedrosis virus (AcNPV; M.D. Summers and G.E. Smith, *A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures* [1986]; Luckow et al., *Bio-technology* 6:47-55 [1987]) for expression of the terpenoid synthases of the invention. Infection of insect cells (such as cells of the species *Spodoptera frugiperda*) with the recombinant baculoviruses allows for the
15 production of large amounts of the monoterpenoid synthase proteins. In addition, the baculovirus system has other important advantages for the production of recombinant (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase. For example, baculoviruses do not infect humans and can therefore be safely handled in large quantities. In the baculovirus system, a DNA construct is prepared including a
20 DNA segment encoding (+)-bornyl diphosphate synthase, (+)-sabinene synthase or 1,8-cineole synthase and a vector. The vector may comprise the polyhedron gene promoter region of a baculovirus, the baculovirus flanking sequences necessary for proper cross-over during recombination (the flanking sequences comprise about 200-300 base pairs adjacent to the promoter sequence) and a bacterial origin of
25 replication which permits the construct to replicate in bacteria. The vector is constructed so that (i) the DNA segment is placed adjacent (or operably linked or "downstream" or "under the control of") to the polyhedron gene promoter and (ii) the promoter/monoterpene synthase combination is flanked on both sides by 200-300 base pairs of baculovirus DNA (the flanking sequences).

30 To produce the monoterpene synthase DNA construct, a cDNA clone encoding the full length (+)-bornyl diphosphate synthase, (+)-sabinene synthase or 1,8-cineole synthase is obtained using methods such as those described herein. The DNA construct is contacted in a host cell with baculovirus DNA of an appropriate baculovirus (that is, of the same species of baculovirus as the promoter encoded in the
35 construct) under conditions such that recombination is effected. The resulting

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recombinant baculoviruses encode the full (+)-bornyl diphosphate synthase, (+)-sabinene synthase or 1,8-cineole synthase. For example, an insect host cell can be cotransfected or transfected separately with the DNA construct and a functional baculovirus. Resulting recombinant baculoviruses can then be isolated and used to
5 infect cells to effect production of the monoterpene synthase. Host insect cells include, for example, *Spodoptera frugiperda* cells, that are capable of producing a baculovirus-expressed monoterpene synthase. Insect host cells infected with a recombinant baculovirus of the present invention are then cultured under conditions allowing expression of the baculovirus-encoded (+)-bornyl diphosphate synthase, (+)-
10 sabinene synthase or 1,8-cineole synthase. (+)-Bornyl diphosphate synthase, (+)-sabinene synthase or 1,8-cineole synthase thus produced are then extracted from the cells using methods known in the art.

Other eukaryotic microbes such as yeasts may also be used to practice this invention. The baker's yeast *Saccharomyces cerevisiae*, is a commonly used yeast,
15 although several other strains are available. The plasmid YRp7 (Stinchcomb et al., *Nature* 282:39 [1979]; Kingsman et al., *Gene* 7:141 [1979]; Tschemper et al., *Gene* 10:157 [1980]) is commonly used as an expression vector in *Saccharomyces*. This plasmid contains the *trp1* gene that provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, such as strains ATCC No. 44,076 and
20 PEP4-1 (Jones, *Genetics* 85:12 [1977]). The presence of the *trp1* lesion as a characteristic of the yeast host cell genome then provides an effective environment for detecting transformation by growth in the absence of tryptophan. Yeast host cells are generally transformed using the polyethylene glycol method, as described by Hinnen (*Proc. Natl. Acad. Sci. USA* 75:1929 [1978]). Additional yeast transformation
25 protocols are set forth in Gietz et al., *N.A.R.* 20(17):1425, 1992; Reeves et al., *FEMS* 99:193-197, 1992.

Suitable promoting sequences in yeast vectors include the promoters for 3-phosphoglycerate kinase (Hitzeman et al., *J. Biol. Chem.* 255:2073 [1980]) or other glycolytic enzymes (Hess et al., *J. Adv. Enzyme Reg.* 7:149 [1968]; Holland et al.,
30 *Biochemistry* 17:4900 [1978]), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase. In the construction of suitable expression plasmids, the termination sequences associated with these genes
35 are also ligated into the expression vector 3' of the sequence desired to be expressed

to provide polyadenylation of the mRNA and termination. Other promoters that have the additional advantage of transcription controlled by growth conditions are the promoter region for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, and the aforementioned
5 glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Any plasmid vector containing yeast-compatible promoter, origin of replication and termination sequences is suitable.

Cell cultures derived from multicellular organisms, such as plants, may be used as hosts to practice this invention. Transgenic plants can be obtained, for example, by
10 transferring plasmids that encode (+)-bornyl diphosphate synthase, (+)-sabinene synthase or 1,8-cineole synthase and a selectable marker gene, e.g., the kan gene encoding resistance to kanamycin, into *Agrobacterium tumefaciens* containing a helper Ti plasmid as described in Hoeckema et al., *Nature* 303:179-181 [1983] and culturing the *Agrobacterium* cells with leaf slices of the plant to be transformed as
15 described by An et al., *Plant Physiology* 81:301-305 [1986]. Transformation of cultured plant host cells is normally accomplished through *Agrobacterium tumefaciens*, as described above. Cultures of mammalian host cells and other host cells that do not have rigid cell membrane barriers are usually transformed using the calcium phosphate method as originally described by Graham and Van der Eb
20 (*Virology* 52:546 [1978]) and modified as described in sections 16.32-16.37 of Sambrook et al., *supra*. However, other methods for introducing DNA into cells such as Polybrene (Kawai and Nishizawa, *Mol. Cell. Biol.* 4:1172 [1984]), protoplast fusion (Schaffner, *Proc. Natl. Acad. Sci. USA* 77:2163 [1980]), electroporation (Neumann et al., *EMBO J.* 1:841 [1982]), and direct microinjection into nuclei
25 (Capecchi, *Cell* 22:479 [1980]) may also be used. Additionally, animal transformation strategies are reviewed in Monastersky G.M. and Robl, J.M., *Strategies in Transgenic Animal Science*, ASM Press, Washington, D.C., 1995. Transformed plant calli may be selected through the selectable marker by growing the cells on a medium containing, e.g., kanamycin, and appropriate amounts of
30 phytohormone such as naphthalene acetic acid and benzyladenine for callus and shoot induction. The plant cells may then be regenerated and the resulting plants transferred to soil using techniques well known to those skilled in the art.

In addition, a gene regulating (+)-bornyl diphosphate synthase, (+)-sabinene synthase or 1,8-cineole synthase production can be incorporated into the plant along
35 with a necessary promoter which is inducible. In the practice of this embodiment of

the invention, a promoter that only responds to a specific external or internal stimulus is fused to the target cDNA. Thus, the gene will not be transcribed except in response to the specific stimulus. As long as the gene is not being transcribed, its gene product is not produced.

5 An illustrative example of a responsive promoter system that can be used in the practice of this invention is the glutathione-S-transferase (GST) system in maize. GSTs are a family of enzymes that can detoxify a number of hydrophobic electrophilic compounds that often are used as pre-emergent herbicides (Weigand et al., *Plant Molecular Biology* 7:235-243 [1986]). Studies have shown that the GSTs are
10 directly involved in causing this enhanced herbicide tolerance. This action is primarily mediated through a specific 1.1 kb mRNA transcription product. In short, maize has a naturally occurring quiescent gene already present that can respond to external stimuli and that can be induced to produce a gene product. This gene has previously been identified and cloned. Thus, in one embodiment of this invention, the promoter
15 is removed from the GST responsive gene and attached to a (+)-bornyl diphosphate synthase, (+)-sabinene synthase or 1,8-cineole synthase gene that previously has had its native promoter removed. This engineered gene is the combination of a promoter that responds to an external chemical stimulus and a gene responsible for successful production of (+)-bornyl diphosphate synthase, (+)-sabinene synthase or 1,8-cineole
20 synthase.

 In addition to the methods described above, several methods are known in the art for transferring cloned DNA into a wide variety of plant species, including gymnosperms, angiosperms, monocots and dicots (see, e.g., Glick and Thompson, eds., *Methods in Plant Molecular Biology*, CRC Press, Boca Raton,
25 Florida [1993]). Representative examples include electroporation-facilitated DNA uptake by protoplasts (Rhodes et al., *Science* 240(4849):204-207 [1988]); treatment of protoplasts with polyethylene glycol (Lyznik et al., *Plant Molecular Biology* 13:151-161 [1989]); and bombardment of cells with DNA laden microprojectiles (Klein et al., *Plant Physiol.* 91:440-444 [1989] and Boynton et al., *Science*
30 240(4858):1534-1538 [1988]). Additionally, plant transformation strategies and techniques are reviewed in Birch, R.G., *Ann Rev Plant Phys Plant Mol Biol* 48:297 (1997); Forester et al., *Exp. Agric.* 33:15-33 (1997). Minor variations make these technologies applicable to a broad range of plant species.

 Each of these techniques has advantages and disadvantages. In each of the
35 techniques, DNA from a plasmid is genetically engineered such that it contains not

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only the gene of interest, but also selectable and screenable marker genes. A selectable marker gene is used to select only those cells that have integrated copies of the plasmid (the construction is such that the gene of interest and the selectable and screenable genes are transferred as a unit). The screenable gene provides another
5 check for the successful culturing of only those cells carrying the genes of interest. A commonly used selectable marker gene is neomycin phosphotransferase II (NPT II). This gene conveys resistance to kanamycin, a compound that can be added directly to the growth media on which the cells grow. Plant cells are normally susceptible to kanamycin and, as a result, die. The presence of the NPT II gene overcomes the
10 effects of the kanamycin and each cell with this gene remains viable. Another selectable marker gene which can be employed in the practice of this invention is the gene which confers resistance to the herbicide glufosinate (Basta). A screenable gene commonly used is the β -glucuronidase gene (GUS). The presence of this gene is characterized using a histochemical reaction in which a sample of putatively
15 transformed cells is treated with a GUS assay solution. After an appropriate incubation, the cells containing the GUS gene turn blue.

The plasmid containing one or more of these genes is introduced into either plant protoplasts or callus cells by any of the previously mentioned techniques. If the marker gene is a selectable gene, only those cells that have incorporated the DNA
20 package survive under selection with the appropriate phytotoxic agent. Once the appropriate cells are identified and propagated, plants are regenerated. Progeny from the transformed plants must be tested to insure that the DNA package has been successfully integrated into the plant genome.

Mammalian host cells may also be used in the practice of the invention.
25 Examples of suitable mammalian cell lines include monkey kidney CVI line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line 293S (Graham et al., *J. Gen. Virol.* 36:59 [1977]); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells (Urlab and Chasin, *Proc. Natl. Acad. Sci USA* 77:4216 [1980]); mouse sertoli cells (TM4, Mather, *Biol. Reprod.* 23:243
30 [1980]); monkey kidney cells (CVI-76, ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); mouse mammary tumor cells (MMT 060562,
35 ATCC CCL 51); rat hepatoma cells (HTC, MI.54, Baumann et al., *J. Cell Biol.* 85:1

[1980]]; and TRI cells (Mather et al., *Annals N.Y. Acad. Sci.* **383**:44 [1982]). Expression vectors for these cells ordinarily include (if necessary) DNA sequences for an origin of replication, a promoter located in front of the gene to be expressed, a ribosome binding site, an RNA splice site, a polyadenylation site, and a transcription terminator site.

Promoters used in mammalian expression vectors are often of viral origin. These viral promoters are commonly derived from polyoma virus, Adenovirus 2, and most frequently Simian Virus 40 (SV40). The SV40 virus contains two promoters that are termed the early and late promoters. These promoters are particularly useful because they are both easily obtained from the virus as one DNA fragment that also contains the viral origin of replication (Fiers et al., *Nature* **273**:113 [1978]). Smaller or larger SV40 DNA fragments may also be used, provided they contain the approximately 250-bp sequence extending from the HindIII site toward the BglII site located in the viral origin of replication.

Alternatively, promoters that are naturally associated with the foreign gene (homologous promoters) may be used provided that they are compatible with the host cell line selected for transformation.

An origin of replication may be obtained from an exogenous source, such as SV40 or other virus (e.g., Polyoma, Adeno, VSV, BPV) and inserted into the cloning vector. Alternatively, the origin of replication may be provided by the host cell chromosomal replication mechanism. If the vector containing the foreign gene is integrated into the host cell chromosome, the latter is often sufficient.

The use of a secondary DNA coding sequence can enhance production levels of (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase in transformed cell lines. The secondary coding sequence typically comprises the enzyme dihydrofolate reductase (DHFR). The wild-type form of DHFR is normally inhibited by the chemical methotrexate (MTX). The level of DHFR expression in a cell will vary depending on the amount of MTX added to the cultured host cells. An additional feature of DHFR that makes it particularly useful as a secondary sequence is that it can be used as a selection marker to identify transformed cells. Two forms of DHFR are available for use as secondary sequences, wild-type DHFR and MTX-resistant DHFR. The type of DHFR used in a particular host cell depends on whether the host cell is DHFR deficient (such that it either produces very low levels of DHFR endogenously, or it does not produce functional DHFR at all). DHFR-deficient cell lines such as the CHO cell line described by Urlaub and Chasin, *supra*, are

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transformed with wild-type DHFR coding sequences. After transformation, these DHFR-deficient cell lines express functional DHFR and are capable of growing in a culture medium lacking the nutrients hypoxanthine, glycine and thymidine. Nontransformed cells will not survive in this medium.

5 The MTX-resistant form of DHFR can be used as a means of selecting for transformed host cells in those host cells that endogenously produce normal amounts of functional DHFR that is MTX sensitive. The CHO-K1 cell line (ATCC No. CL 61) possesses these characteristics, and is thus a useful cell line for this purpose. The addition of MTX to the cell culture medium will permit only those cells transformed
10 with the DNA encoding the MTX-resistant DHFR to grow. The nontransformed cells will be unable to survive in this medium.

Prokaryotes may also be used as host cells for the initial cloning steps of this invention. They are particularly useful for rapid production of large amounts of DNA, for production of single-stranded DNA templates used for site-directed mutagenesis,
15 for screening many mutants simultaneously, and for DNA sequencing of the mutants generated. Suitable prokaryotic host cells include *E. coli* K12 strain 94 (ATCC No. 31,446), *E. coli* strain W3110 (ATCC No. 27,325) *E. coli* X1776 (ATCC No. 31,537), and *E. coli* B; however many other strains of *E. coli*, such as HB101, JM101, NM522, NM538, NM539, and many other species and genera of prokaryotes
20 including bacilli such as *Bacillus subtilis*, other enterobacteriaceae such as *Salmonella typhimurium* or *Serratia marcesans*, and various *Pseudomonas* species may all be used as hosts. Prokaryotic host cells or other host cells with rigid cell walls are preferably transformed using the calcium chloride method as described in section 1.82 of Sambrook et al., *supra*. Alternatively, electroporation may be used for
25 transformation of these cells. Prokaryote transformation techniques are set forth in Dower, W. J., in Genetic Engineering, Principles and Methods, 12:275-296, Plenum Publishing Corp., 1990; Hanahan et al., *Meth. Enzymol.*, 204:63, 1991.

As a representative example, cDNA sequences encoding (+)-bornyl diphosphate synthase, (+)-sabinene synthase or 1,8-cineole synthase may be
30 transferred to the (His)₆-Tag pET vector commercially available (from Novagen) for overexpression in *E. coli* as heterologous host. This pET expression plasmid has several advantages in high level heterologous expression systems. The desired cDNA insert is ligated in frame to plasmid vector sequences encoding six histidines followed by a highly specific protease recognition site (thrombin) that are joined to the amino
35 terminus codon of the target protein. The histidine "block" of the expressed fusion

protein promotes very tight binding to immobilized metal ions and permits rapid purification of the recombinant protein by immobilized metal ion affinity chromatography. The histidine leader sequence is then cleaved at the specific proteolysis site by treatment of the purified protein with thrombin, and the (+)-bornyl
5 diphosphate synthase, (+)-sabinene synthase or 1,8-cineole synthase again purified by immobilized metal ion affinity chromatography, this time using a shallower imidazole gradient to elute the recombinant synthases while leaving the histidine block still adsorbed. This overexpression-purification system has high capacity, excellent resolving power and is fast, and the chance of a contaminating *E. coli* protein
10 exhibiting similar binding behavior (before and after thrombin proteolysis) is extremely small.

As will be apparent to those skilled in the art, any plasmid vectors containing replicon and control sequences that are derived from species compatible with the host cell may also be used in the practice of the invention. The vector usually has a
15 replication site, marker genes that provide phenotypic selection in transformed cells, one or more promoters, and a polylinker region containing several restriction sites for insertion of foreign DNA. Plasmids typically used for transformation of *E. coli* include pBR322, pUC18, pUC19, pUC118, pUC119, and Bluescript M13, all of which are described in sections 1.12-1.20 of Sambrook et al., *supra*. However, many
20 other suitable vectors are available as well. These vectors contain genes coding for ampicillin and/or tetracycline resistance which enables cells transformed with these vectors to grow in the presence of these antibiotics.

The promoters most commonly used in prokaryotic vectors include the β -lactamase (penicillinase) and lactose promoter systems (Chang et al. *Nature*
25 375:615 [1978]; Itakura et al., *Science* 198:1056 [1977]; Goeddel et al., *Nature* 281:544 [1979]) and a tryptophan (trp) promoter system (Goeddel et al., *Nucl. Acids Res.* 8:4057 [1980]; EPO Appl. Publ. No. 36,776), and the alkaline phosphatase systems. While these are the most commonly used, other microbial promoters have been utilized, and details concerning their nucleotide sequences have been published,
30 enabling a skilled worker to ligate them functionally into plasmid vectors (see Siebenlist et al., *Cell* 20:269 [1980]).

Many eukaryotic proteins normally secreted from the cell contain an endogenous secretion signal sequence as part of the amino acid sequence. Thus, proteins normally found in the cytoplasm can be targeted for secretion by linking a
35 signal sequence to the protein. This is readily accomplished by ligating DNA

encoding a signal sequence to the 5' end of the DNA encoding the protein and then expressing this fusion protein in an appropriate host cell. The DNA encoding the signal sequence may be obtained as a restriction fragment from any gene encoding a protein with a signal sequence. Thus, prokaryotic, yeast, and eukaryotic signal sequences may be used herein, depending on the type of host cell utilized to practice the invention. The DNA and amino acid sequence encoding the signal sequence portion of several eukaryotic genes including, for example, human growth hormone, proinsulin, and proalbumin are known (see Stryer, *Biochemistry* W.H. Freeman and Company, New York, NY, p. 769 [1988]), and can be used as signal sequences in appropriate eukaryotic host cells. Yeast signal sequences, as for example acid phosphatase (Arima et al., *Nuc. Acids Res.* 11:1657 [1983]), α -factor, alkaline phosphatase and invertase may be used to direct secretion from yeast host cells. Prokaryotic signal sequences from genes encoding, for example, LamB or OmpF (Wong et al., *Gene* 68:193 [1988]), MalE, PhoA, or beta-lactamase, as well as other genes, may be used to target proteins from prokaryotic cells into the culture medium.

As described above, the (+)-bornyl diphosphate synthase, 1,8-cineole synthase and (+)-sabinene synthase amino terminal membrane insertion sequences reside at SEQ ID No:2, amino acids 1 through 56; SEQ ID No:4, amino acids 1 through 58; SEQ ID No:6, amino acids 1 through 53) and direct the enzymes to plastids. Alternative trafficking sequences from plants, animals and microbes can be employed in the practice of the invention to direct the gene product to the cytoplasm, endoplasmic reticulum, mitochondria or other cellular components, or to target the protein for export to the medium. These considerations apply to the overexpression of (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase, and to direction of expression within cells or intact organisms to permit gene product function in any desired location.

The construction of suitable vectors containing DNA encoding replication sequences, regulatory sequences, phenotypic selection genes and the monoterpene synthase DNA of interest are prepared using standard recombinant DNA procedures. Isolated plasmids and DNA fragments are cleaved, tailored, and ligated together in a specific order to generate the desired vectors, as is well known in the art (see, for example, Maniatis, *supra*, and Sambrook et al., *supra*).

As discussed above, (+)-bornyl diphosphate synthase, (+)-sabinene synthase and 1,8-cineole synthase variants are preferably produced by means of mutation(s) that are generated using the method of site-specific mutagenesis. This method

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requires the synthesis and use of specific oligonucleotides that encode both the sequence of the desired mutation and a sufficient number of adjacent nucleotides to allow the oligonucleotide to stably hybridize to the DNA template.

The foregoing may be more fully understood in connection with the following representative examples, in which "Plasmids" are designated by a lower case p followed by an alphanumeric designation. The starting plasmids used in this invention are either commercially available, publicly available on an unrestricted basis, or can be constructed from such available plasmids using published procedures. In addition, other equivalent plasmids are known in the art and will be apparent to the ordinary artisan.

"Digestion", "cutting" or "cleaving" of DNA refers to catalytic cleavage of the DNA with an enzyme that acts only at particular locations in the DNA. These enzymes are called restriction endonucleases, and the site along the DNA sequence where each enzyme cleaves is called a restriction site. The restriction enzymes used in this invention are commercially available and are used according to the instructions supplied by the manufacturers. (See also sections 1.60-1.61 and sections 3.38-3.39 of Sambrook et al., *supra*.)

"Recovery" or "isolation" of a given fragment of DNA from a restriction digest means separation of the resulting DNA fragment on a polyacrylamide or an agarose gel by electrophoresis, identification of the fragment of interest by comparison of its mobility versus that of marker DNA fragments of known molecular weight, removal of the gel section containing the desired fragment, and separation of the gel from DNA. This procedure is known generally. For example, see Lawn et al. (*Nucleic Acids Res.* 9:6103-6114 [1982]), and Goeddel et al. (*Nucleic Acids Res.*, *supra*).

The following examples merely illustrate the best mode now contemplated for practicing the invention, but should not be construed to limit the invention. All literature citations herein are expressly incorporated by reference.

EXAMPLES

Example 1

cDNA Library Construction and Cloning of Monoterpene Synthases

cDNA Library Preparation, Sage plants (*S. officinalis* L.) were grown from seed as previously described (Croteau, R., and Karp, F., *Arch. Biochem. Biophys.* 198:512-522, 1979). Approximately 15 g of emerging sage leaves (shoot tips) from three-week-old plants were ground to a fine powder in liquid nitrogen and extracted

into buffer composed of 200 mM Tris-HCl (pH 8.5), 300 mM LiCl and 10 mM EDTA, and containing 1% (w/v) polyvinylpyrrolidone (M_r ~40,000). The high concentration of chloride salts and high pH were empirically optimized to maximize the yield of intact RNA, and polyvinylpyrrolidone was found to be essential to complex co-extracted oils, resins and phenolic substances that otherwise prevent RNA isolation. Total RNA thus extracted was prepared by precipitation with isopropanol, followed by CsCl density gradient centrifugation, as previously described (Lewinsohn et al., *Plant Mol. Biol. Rep.* 12:20-25, 1994). Poly(A)⁺ mRNA was isolated by chromatography on oligo(dT)-cellulose (Qiagen) and 6.3 µg of the resulting mRNA was used to construct a Σ ZAPII cDNA library according to the manufacturer's instructions (Stratagene).

PCR-Based Probe Generation and Library Screening Protein purification from sage, as the basis for cDNA isolation, has been of limited success (McGeary, P., and Croteau, R., *Arch. Biochem. Biophys.* 317:149-155, 1995) because of the number of synthases present and their similarity in physical properties (Alonso, W. R., and Croteau, R., in *Methods in Plant Biochemistry (Enzymes of Secondary Metabolism)* (Lea, P. J., ed) Vol. 9, pp. 239-260, Academic Press, New York, 1993), and thus far has not permitted a reverse genetic approach to cloning of any of the monoterpene synthases from this species. Consequently, a generic strategy for the homology-based PCR cloning of terpenoid synthases of higher plant origin was utilized (Steele et al., *Proc. Natl. Acad. Sci. USA* 92:4164-4168, 1995), in this instance by comparing monoterpene synthase cDNA sequences that were isolated from both angiosperms and gymnosperms (Colby et al., *J. Biol. Chem.* 268:23016-23024, 1993; Yuba et al., *Arch. Biochem. Biophys.* 332:280-287, 1996; Bohlmann et al., *J. Biol. Chem.* 272:21784-21792, 1997).

Three PCR oligonucleotide primers were synthesized based on the results of the monoterpene synthase homology comparison:

1F 5'AA(G/A)AA(T/C)GA(G/A)(G/A)A(G/A)GGIGAITA(C/T)AA(G/A)GA-3'
(SEQ ID No:8)

30 2F 5'-(T/C)TICA(G/A)(C/T)TITA(T/C)GA(G/A)GC-3' (SEQ ID No:9)

3R 5'-CT(A/G)GT(C/T)(G/A)AIGGI(C/A)T(G/A)AT(G/A)TACGT(C/T)-3'
(SEQ ID No:10)

Each of the sense primers (1F and 2F) was used for PCR in combination with antisense primer (3R). Using purified sage leaf cDNA library phage as template (5 µl at 1.5×10^9 plaque forming units/ml), PCR was performed in a total volume of 50 µl

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containing 20 mM Tris-HCl (pH 8.4), 50 mM KCl, 5 mM MgCl₂, 200 µM of each dNTP, 5 µM of each primer and 2.5 units of *Taq* polymerase (BRL or Life Sciences). The thermal cycler performed the following denaturation, annealing and amplification steps: denaturation at 94°C, 1 minute; annealing at 60°C, 1 minute; extension at 72°C, 3.5 minutes; 35 cycles with final extension at 72°C, five minutes. Analysis of the PCR reaction products by agarose gel electrophoresis (Sambrook, J., Fritsch, E. F., and Maniatis, T. (1989) *Molecular Cloning: A Laboratory Manual*, 2nd Ed., pp. 2.69-2.76, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY) indicated that only the combination of primers 2F and 3R amplified a discrete product of approximately 600 bp, which was gel purified, ligated into pT7Blue (Novagen), and transformed into *E. coli* NovaBlue cells. Plasmid DNA was prepared from 32 individual transformants and the inserts partially sequenced (DyeDeoxy Terminator Cycle Sequencing; Applied Biosystems) to reveal that two distinct "terpenoid synthase-like" sequences had been amplified in roughly comparable amounts (SEQ ID No:11 and SEQ ID No:12).

The relative ability of these two potential probes to hybridize with expressed genes was evaluated by RNA-DNA hybridization. Two samples of sage leaf mRNA isolated as above (3 µg each) were electrophoresed on 1% (w/v) agarose under denaturing conditions and blotted onto separate PVDF membranes using standard techniques (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., pp. 2.69-2.76, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989). Each membrane was evaluated with ³²P labeled probe, generated from one or the other of the 600 bp fragments using random hexamer priming (Tabor et al., *Current Protocols in Molecular Biology* (Ausubel et al., eds), sections 3.5.9-3.5.10, John Wiley & Sons, New York, 1991), by standard hybridization and washing protocols (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., pp. 2.69-2.76, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989). Autoradiography of the membrane revealed that both probes hybridized to a 2 kb transcript, although one probe (SEQ ID No:11) generated a significantly stronger signal (~10-fold) than the other (SEQ ID No:12). The probe generating the stronger signal (SEQ ID No:11) was subsequently employed to screen the cDNA library in an attempt to isolate full-length cDNA sequences encoding the corresponding terpene synthase.

UV-crosslinked nitrocellulose lifts containing 3-5 x 10⁴ primary plaques (plated on *E. coli* XL1-Blue-MRF'), after pre-hybridization (in 1.25 x SSPE, 0.5 x Denhart's reagent, 9% formamide, 0.002% SDS, and 10 µg/ml denatured *E. coli*

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DNA, for 2 h at 42°C), were hybridized in the same medium with approximately 8 μ Ci of the 32 P labeled probe for 48 h. Filters were washed, first at room temperature (in 2 x SSC with 0.1% SDS), then at 55°C (in 1 x SSC with 0.1% SDS), and subsequently exposed to X-ray film at -70°C (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., pp. 2.69-2.76, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989). Plaques yielding positive signals were purified through two additional rounds of hybridization. A total of 77 purified Σ ZAP clones so isolated were excised *in vivo* to generate BluescriptII SK(-) phagmids and transformed into *E. coli* XL0LR cells according to the Stratagene protocol. The size of each cDNA insert was determined by PCR using T3 and T7 primers, and transformed clones containing an insert >1.6 kb were either expressed to assay for monoterpene synthase activity or sequenced at the 5'-terminus using the T3 promoter primer. Bluescript plasmids expressing synthase activity in cell-free extracts of transformed *E. coli* (see Examples 2 and 3) were fully sequenced on both DNA strands by primer walking or by the method of nested deletions using exonuclease III and mung bean nuclease (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., pp. 2.69-2.76, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989).

To improve functional expression and facilitate subsequent enzyme purification, each of the apparent full-length pBluescript clones that expressed monoterpene synthase activity was subcloned in frame into pGEX vectors (Pharmacia) using a convenient *Bam*HI (SBC and SSS) or *Eco*RI (SCS) restriction site at the 5'-end, and the *Xho*I restriction site at the 3'-terminus. Fidelity in subcloning was confirmed by complete sequencing, and these plasmid constructs were expressed in *E. coli* XL1-Blue-MFR' cells.

Example 2

Expression of Monoterpene Synthase cDNAs in *E. coli*

The bluescript plasmids expressed in *E. coli* strain XL1-Blue were grown in 5 ml LB medium (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., pp. 2.69-2.76, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989), supplemented with 100 μ g ampicillin/ml, to an $A_{600} = 0.5$ at 37°C with constant shaking, then induced with 1 to 3 mM IPTG. The cells were allowed an additional 4 h growth at 37°C before harvesting by centrifugation (2000 x g, 10 min) and lysis by sonication (Braun-Sonic 2000 with microprobe at maximum power for 15 seconds), on ice, in 50 mM Mopso buffer containing 10% glycerol, 10 mM $MgCl_2$

and 5 mM DTT (pH either 6.5 or 7.1, as appropriate). The sonicates were cleared by centrifugation (18,000 x g, 10 min) and the resulting supernatant was used as the enzyme source. The pGEX constructs in *E. coli* XLI-Blue-MFR' cells were similarly grown at 37°C to $A_{600} = 1.0$ to 1.5, then induced with 1 mM IPTG and incubated
5 overnight at 20°C with constant shaking. The cells were then harvested and lysed, and the soluble supernatant prepared as before. Purification of the resulting fusion proteins was attempted using the glutathione-Sepharose affinity column according to the manufacturer's instructions (Pharmacia).

Of the three expressed monoterpene synthases (SBS, SCS and SSS), only one
10 (SBS) bound to the matrix but, even in this case, affinity-based purification proved to be unreliable. Therefore, partial purification of the heterologously expressed synthases was achieved by ion-exchange chromatography on DEAE-cellulose (Whatman DE-52) using a 0-400 mM NaCl gradient. The partially purified preparations were desalted by repeated ultrafiltration and dilution using an Amicon
15 Centriprep 30 concentrator (30 kDa cutoff) and the appropriate assay buffer. The pGEX-expressed fusion proteins were also subjected to gel permeation chromatography (Pharmacia FPLC system) using a Pharmacia XY 16 x 70 column packed with Superdex S-200 and equilibrated with the appropriate 50 mM Mopso buffer system. The column was developed at a flow rate of 0.3 ml per min and was
20 calibrated using the Sigma MW-GF-200 molecular weight marker kit. K_{av} values of the recombinant enzymes were compared to the calibration standards to establish molecular weights (Cooper, T. G. *The Tools of Biochemistry*, John Wiley & Sons, New York, 1977), which were then corrected for the engineered fusion and transit peptide to estimate the molecular weight of the corresponding native form.

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Example 3

Monoterpene Synthase Assays and Product Identification

Monoterpene Synthase Assays. [$1\text{-}^3\text{H}$]Geranyl diphosphate (250 Ci/mol) was prepared by an established method (Croteau et al., *Arch. Biochem. Biophys.* **309**:184-192, 1994). Terpenoid standards were from our own collection. Unless otherwise
30 stated, all reagents were obtained from Sigma Chemical Co. or Aldrich Chemical Co.

Monoterpene synthase activities were assayed by methods previously described (Croteau, R., and Karp, F., *Arch. Biochem. Biophys.* **198**:512-522, 1979; Croteau et al., *Arch. Biochem. Biophys.* **309**:184-192, 1994; Gambliel, H., and Croteau, R., *J. Biol. Chem.* **259**:740-748, 1984; Croteau, R., and Cane, D.E.,
35 *Methods Enzymol.* **110**:383-405, 1985). Briefly, an aliquot of the bacterial cell lysate,

appropriate column fractions, or partially purified and desalted enzyme preparation, in 0.5 or 1.0 ml of 50 mM Mopso buffer (pH 6.1 to 7.0, as appropriate for the target activity) containing 10 mM MgCl_2 , 5 mM DTT and 10% (v/v) glycerol, was transferred to a 7 ml glass, Teflon sealed, screw-capped tube, and the mixture was
5 overlaid with 1 ml pentane to trap volatile products. The reaction was initiated by the addition of 4.5 μM [$1\text{-}^3\text{H}$]geranyl diphosphate (1.3 μCi), with incubation at 31°C with gentle shaking for 0.5 to 3.0 h. The pentane layer and an additional pentane extract (2 x 1 ml) were passed over a short column of silica gel surmounted by anhydrous MgSO_4 (in a Pasteur pipette) to afford the monoterpene olefin fraction.
10 Subsequent extraction of the remaining aqueous phase with diethyl ether (2 x 1 ml), and passage of this extract through the same column, yielded the oxygenated monoterpene fraction. The residual aqueous phase was then treated with excess potato apyrase and wheat germ acid phosphatase to hydrolyze monoterpenol diphosphate esters (Croteau, R., and Karp, F., *Arch. Biochem. Biophys.* **198**:512-522,
15 1979; Croteau, R., and Cane, D.E., *Methods Enzymol.* **110**:383-405, 1985). The liberated alcohols were then extracted into diethyl ether (2 x 1 ml) and the combined extract dried over anhydrous MgSO_4 . Radioactivity in the various fractions was determined by liquid scintillation counting of aliquots (Packard 460 CD with external standard quench correction) and the remaining material was concentrated for radio-
20 GC and GC-MS analysis.

Kinetic analyses were carried out with the partially purified, recombinant pGEX fusion proteins by determination of initial reaction rates at a minimum of ten substrate concentrations ranging from 0.45 to 45 μM [$1\text{-}^3\text{H}$]geranyl diphosphate, at saturating levels of the divalent metal ion cofactor. The results were analyzed by non-
25 linear regression of the Michaelis-Menten equation using the curve-fitting capabilities of Sigma-Plot (Jandel Corp.).

Product Identification - To obtain sufficient product for analysis by radio-GC and chiral phase capillary GC-MS, the samples from multiple assays were pooled as necessary. Radio-GC was performed on a Gow-Mac 550P gas chromatograph with
30 thermal conductivity detector directly coupled to a Packard 894 gas proportional counter (30). An AT-1000 packed column (Alltech) was used with He as carrier at 30 ml/min and with temperature programming from 70°C to 200°C (at 5°C/min) for analysis of monoterpene olefins, and from 100°C to 200°C (at 5°C/min) for analysis of oxygenated monoterpenes. Authentic standards (10-20 μg /component) were

included with each injection in order to correlate retention times determined by mass and radioactivity detectors.

GC-MS was performed on a Hewlett-Packard 6890 GC-quadrupole mass selective detector system interfaced with a Hewlett-Packard Chemstation for data analysis. Chiral phase separations were performed by split injection (25:1) on a 30 m cyclodex-B capillary column (J&W Scientific) using He as carrier at 0.6 ml/min and temperature programming from 35°C to 200°C at 10°C/min.

Example 4

Product Profiles of Recombinant Synthases

Since the formation of multiple products from geranyl diphosphate is a common, if unusual, feature of the monoterpene synthases (Croteau, R., *Chem. Rev.* 87:929-954, 1987; Wise, M. L., and Croteau, R., in *Comprehensive Natural Products Chemistry: Isoprenoids* (Cane, D. E., ed) Vol. 2 (in press), Elsevier Science, Oxford, 1998), the product profiles of the recombinant enzymes were examined in detail by radio-GC and GC-MS. Recombinant sabinene synthase (SSS) produces exclusively monoterpene olefins, which by radio-GC were identified as sabinene (62%), K-terpinene (21%), terpinolene (6.7%), limonene (6.5%) and myrcene (2.5%). The major products of this enzyme (sabinene and K-terpinene) are formed by a cyclization mechanism involving a 1,2-hydride shift in the α -terpinyl cation intermediate. Chiral phase capillary GC-MS demonstrated the biosynthetic sabinene to be coincident with authentic (+)-sabinene; however, the (-)-enantiomer was not available for analysis to confirm the absolute configuration of this product. Previous studies have shown that cell-free extracts from sage produce only the (+)-antipode of sabinene from geranyl diphosphate (Croteau, R., in *Recent Developments in Flavor and Fragrance Chemistry* (Hopp, R., and Mori, K., eds), pp. 263-273, VCH, Weinheim, Germany, 1992; Croteau, R., in *Flavor Precursors: Thermal and Enzymatic Conversions* (Teranishi, R., Takeoka, G. R., and Guntert, M., eds), American Chemical Society Symposium Series, No. 490, pp. 8-20, Washington, DC, 1992), supporting the assignment of the (+)-stereoisomer in this case. The other principal olefinic products of SSS are achiral.

Cineole synthase (SCS) was shown by aliquot counting and radio-GC of the various metabolite fractions to produce both oxygenated monoterpenes (1,8-cineole, 79%, with a few percent α -terpineol) and a mixture of olefins (~20%). Chiral phase capillary GC-MS allowed resolution, confirmation and quantification of the olefins as (+)- α -pinene (5.5% of total products), (-)- α -pinene (0.9%), myrcene (2.9%),

sabinene (2.6%, presumably the (+)-enantiomer), (+)- β -pinene (2.7%), (-)- β -pinene (4.1%), (+)-limonene (1.1%) and (-)-limonene (0.4%). The stereochemistry of the enzymatic transformation leading to 1,8-cineole has been examined (Croteau et al., *Arch. Biochem. Biophys.* 309:184-192, 1994) and shown to involve the cyclization of the bound intermediate 3*R*-linalyl diphosphate in *anti,endo*-conformation, i.e., the same overall stereochemistry required for the production of (+)- α -pinene, (+)- β -pinene and (+)-limonene (Gambliel, H., and Croteau, R., *J. Biol. Chem.* 259:740-748, 1984). The formation of the (-)-series of antipodes must therefore occur via the extended (*anti,exo*) conformation. This apparent loss of stereochemical fidelity in the production of some of the olefin by-products may be a consequence of the fact that the enzyme is expressed as the pGEX fusion of the preprotein of the native synthase, and thus bears a large amino-terminal extension that could compromise substrate and intermediate binding conformations.

Bornyl diphosphate synthase (SBS) was shown, by radio-GC evaluation of all metabolite fractions, to produce principally bornyl diphosphate (75%), as demonstrated by enzymatic hydrolysis of this product followed by separation of the derived borneol from the residual geraniol (liberated from the substrate) and from lesser amounts of non-enzymatic solvolysis products (also generated from geranyl diphosphate in the course of the analysis). The production of bornyl diphosphate by this recombinant enzyme was also demonstrated directly by radio-HPLC analysis of the aqueous reaction mixture using an ion-pairing, reversed-phase chromatography protocol previously established for the separation of prenyl diphosphate esters (McCaskill, D., and Croteau, R., *Anal. Biochem.* 215:142-149, 1993). Additionally, chiral phase capillary GC-MS analysis of the derived borneol demonstrated the exclusive presence of the (+)-antipode, as expected based on studies with the corresponding native enzyme (Croteau, R., and Karp, F., *Arch. Biochem. Biophys.* 198:512-522, 1979; Croteau et al., *J. Biol. Chem.* 260:5956-5962, 1985; Croteau et al., *J. Biol. Chem.* 261:13438-13445, 1986).

The recombinant (+)-bornyl diphosphate synthase was also shown, by radio-GC of the olefin fraction and chiral phase GC analysis, to produce a series of olefins (25% of total product) identified as (+)- α -pinene (3.4% of total product), (+)-camphene (9.5%), (-)-camphene (0.5%), (+)-limonene (3.9%), (-)-limonene (3.9%), terpinolene (2.1%) and myrcene (1.5%). Since formation of the (+)-olefin series is mechanistically related to the formation of (+)-bornyl diphosphate via the *anti,endo*-cyclization of the intermediate 3*R*-linalyl diphosphate (Croteau et al., *J.*

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Biol. Chem. 264:2075-2080, 1989; Croteau et al., *J. Biol. Chem.* 260:5956-5962, 1985; Croteau et al., *J. Biol. Chem.* 261:13438-13445, 1986; Croteau et al., *J. Biol. Chem.* 263:10063-10071, 1988; Croteau et al., *Arch. Biochem. Biophys.* 277:374-381, 1990), the generation of small amounts of the antipodal (-)-camphene and (-)-limonene by the recombinant cyclase again suggests some loss of stereochemical fidelity in the overall reaction sequence.

Example 5

Sequence Analysis of Recombinant Synthases

DNA sequences were assembled and analyzed using GCG software (Wisconsin Package version 9.0, Genetics Computer Group (GCG), Madison, WI). Alignment of the deduced amino acid sequences of SBS clone 3C6 (SEQ ID No:1) (2025 bps, with an ORF of 1794 nts encoding 598 amino acids for a protein of 69.3 kDa and calculated pI of 6.06), SCS clone 3B5 (SEQ ID No:3) (1968 bps, with an ORF of 1773 nts encoding 591 amino acids for a protein of 69.4 kDa and calculated pI of 5.79), and SSS clone 3F25 (SEQ ID No:5) (1911 bps, with an ORF of 1767 nts encoding 589 amino acids for a protein of 68.9 kDa and calculated pI of 5.22), with the published sequences for (-)-limonene synthase from *Mentha spicata* (spearmint) (Colby et al., *J. Biol. Chem.* 268:23016-23024, 1993) and *Perilla frutescens* (Yuba et al., *Arch. Biochem. Biophys.* 332:280-287, 1996), linalool synthase from *Clarkia breweri* (Dudareva et al., *Plant Cell* 8:1137-1148, 1996), and three monoterpene olefin synthases from *Abies grandis* (grand fir) (Bohlmann et al., *J. Biol. Chem.* 272:21784-21792, 1997), illustrates that there are several regions of similarity between these nine monoterpene synthases of diverse origin. Comparison of these sequences using the GCG GAP program (Wisconsin Package version 9.0, Genetics Computer Group (GCG), Madison, WI) revealed the monoterpene synthases from sage to resemble each other and the limonene synthases from related members of the Lamiaceae (50-70% identity, 70-85% similarity) more closely than the monoterpene synthases of the gymnosperm grand fir (-32% identity) or the linalool synthase from *C. breweri* (-25% identity).

Monoterpene biosynthesis is compartmentalized in plastids (Gleizes et al., *Planta* 159:373-381, 1983; Mettal et al., *Eur. J. Biochem.* 170:613-616, 1988; Perez et al., *Plant Physiol. Biochem.* 28:221-229, 1990), thus the monoterpene synthases are encoded as preproteins bearing an amino-terminal transit peptide for import of these nuclear gene products into plastids (leucoplasts of the oil gland cells in the present instance) where they are proteolytically processed to the mature forms

(Keegstra et al., *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 40:471-501, 1989). In all of the monoterpene synthases thus far examined, the 50 to 60 amino terminal residues are characterized by a low degree of similarity, typical of targeting sequences, yet they all share common features of transit peptides in being rich in serine, threonine and
5 small hydrophobic residues but with few acidic residues (Keegstra et al., *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 40:471-501, 1989; von Heijne et al., *Eur. J. Biochem.* 180:535-545, 1989).

All native monoterpene synthases thus far examined appear to be *N*-terminally blocked, preventing direct determination (by sequencing) of the transit peptide-mature
10 protein cleavage junction (Lewinsohn et al., *Arch. Biochem. Biophys.* 293:167-173, 1992; McGeady, P., and Croteau, R., *Arch. Biochem. Biophys.* 317:149-155, 1995; Steele et al., *Proc. Natl. Acad. Sci. USA* 92:4164-4168, 1995; Colby et al., *J. Biol. Chem.* 268:23016-23024, 1993). Significantly, a tandem pair of arginine residues (e.g., arg⁵⁵ arg⁵⁶ of SBS, arg⁵⁷ arg⁵⁸ of SCS and arg⁵² arg⁵³ of SSS) are strictly
15 conserved in the deduced sequences of all of the monoterpene synthases and they define the most *N*-terminal region of obvious homology, suggesting a possible cleavage site. It is believed that truncation of the recombinant (+)-bornyl diphosphate synthase, 1,8-cineole synthase and (+)-sabinene synthase preproteins immediately upstream of these tandem arginines will yield fully functional "pseudomature" forms
20 of the enzymes, whereas truncation downstream from this element will severely impair activity.

Downstream of the aforementioned, tandem arginines are several regions of homology, including the universally conserved (I,L or V)DDXXD (SEQ ID No:13) motif (e.g., residues I³⁵⁰-D³⁵⁵ of SBS) (SEQ ID No:2) found in virtually all deduced
25 sequences for enzymes that utilize prenyl diphosphate substrates (Chen et al., *Protein Sci.* 3:600-607, 1994; Chen et al., *Arch. Biochem. Biophys.* 324:255-266, 1995). This aspartate rich element is now generally recognized as a binding site for the metal ion chelated diphosphate ester substrate (Chen et al., *Protein Sci.* 3:600-607, 1994; Ashby, M. N., and Edwards, P. A., *J. Biol. Chem.* 265:13157-13164, 1990; Tarshis
30 et al., *Biochemistry* 33:10871-10877, 1994; Cane et al., *Biochemistry* 33:5846-5857, 1994; Tarshis et al., *Proc. Natl. Acad. Sci. USA* 93:15018-15023, 1996). Several other highly conserved regions are also apparent including, with reference to the amino acid sequence of SBS (SEQ ID No:2): Arg²⁹⁸-Trp-Trp³⁰⁰, Arg³⁷²-Trp-Glu/Gln³⁷⁴, Tyr³⁸⁴-Met-Gln/Lys³⁸⁶ and Cys⁵¹⁶-Tyr-Met-X-Glu/Asp⁵²⁰ (SEQ ID
35 No:14). The active site peptide LQLYEASFLI (SEQ ID No:15), previously isolated

from the co-purified (+)-pinene synthase and (+)-bornyl diphosphate synthase of sage (McGeady, P., and Croteau, R., *Arch. Biochem. Biophys.* 317:149-155, 1995) was located at residues 195-204 of SBS (SEQ ID No:2) and also at residues 187-196 of SSS (SEQ ID No:6). Very similar sequences in the same location were found in SCS (SEQ ID No:4, amino acid residues 191-200) and in the two limonene synthase sequences from *M. spicata* and *P. frutescens*.

The (+)-bornyl diphosphate synthase from sage has previously been shown to be inhibited by the 'active serine'-directed reagent diisopropylfluorophosphate (Croteau, R., and Karp, F., *Arch. Biochem. Biophys.* 198:512-522, 1979), a characteristic not shared by other monoterpene cyclases (Alonso, W. R., and Croteau, R., in *Methods in Plant Biochemistry (Enzymes of Secondary Metabolism)* (Lea, P.J., ed) Vol. 9, pp. 239-260, Academic Press, New York, 1993). Because of the unique utilization of the substrate diphosphate moiety as the terminating nucleophile by this enzyme (Cane et al., *J. Am. Chem. Soc.* 104:5831-5833, 1982; Croteau et al., *Biochemistry* 24:7077-7085, 1985), it was hypothesized that a serine residue may be involved in binding and transfer of the diphosphate function in the course of the reaction. Sequence comparison of SBS with the other two monoterpene synthases of sage reveals four unique serine residues at positions 302, 320, 454 and 469 (SEQ ID No:2). Two (at positions 302 and 320) are within otherwise highly conserved regions and are, therefore, obvious targets for selective covalent modification with radiolabeled diisopropylfluorophosphate and directed mutagenesis studies.

Example 6

Physical Properties of Recombinant Synthases

Properties of SBS Calibrated gel permeation chromatography of the pGEX fusion form of SBS revealed a single peak of activity at an elution volume corresponding to an M_r ~200,000, indicating that the expressed fusion preprotein (corresponding to a molecular weight of about 2 x 96,300) was a functional dimer. Treatment of the SBS protein with thrombin to remove the glutathione-S-transferase fusion tag, followed by re-chromatography, indicated a decrease in molecular weight to approximately 135,000, consistent with the loss of the 27 kDa transferase peptide from each subunit at a calculated molecular weight of 69,300 for the preprotein. Further correction of the molecular weight to account for the transit peptide would yield a dimer of about 120 kDa which corresponds roughly to the native dimer molecular weight of both (+)-bornyl diphosphate synthase and (+)-pinene synthase

from sage (Croteau, R., and Karp, F., *Arch. Biochem. Biophys.* **198**:512-522, 1979 ; Gambliel, H., and Croteau, R., *J. Biol. Chem.* **259**:740-748, 1984), two enzymes which have never been satisfactorily resolved as distinct species. Although a dimeric quarternary structure is not unique to these two synthases, the vast majority of the
5 monoterpenes synthases characterized to date are monomeric (Alonso, W. R., and Croteau, R., in *Methods in Plant Biochemistry (Enzymes of Secondary Metabolism)* (Lea, P. J., ed) Vol. 9, pp. 239-260, Academic Press, New York, 1993).

The product profile of the protein encoded by SBS clone 3C6 (SEQ ID No:2) is qualitatively similar to the combination of both (+)-bornyl diphosphate synthase and
10 (+)-pinene synthase (i.e., (+)-bornyl diphosphate and the (+)-series of α -pinene and related olefins) (Croteau, R., and Karp, F., *Arch. Biochem. Biophys.* **198**:512-522, 1979; Gambliel, H., and Croteau, R., *J. Biol. Chem.* **259**:740-748, 1984), although the quantitative distributions do not exactly match, and the stereochemistry of the olefin products is anomalous. Thus, (+)-bornyl diphosphate and (+)- α -pinene,
15 (+)-camphene and (+)-limonene arise via the same overall cyclization stereochemistry, and these enantiomers are produced exclusively from geranyl diphosphate by the native (+)-bornyl diphosphate and (+)-pinene synthase activities (Croteau et al., *J. Biol. Chem.* **264**:2075-2080, 1989; Croteau et al., *J. Biol. Chem.* **260**:5956-5962, 1985; Croteau et al., *J. Biol. Chem.* **261**:13438-13445, 1986; Croteau et al., *J. Biol.*
20 *Chem.* **263**:10063-10071, 1988; Croteau et al., *Arch. Biochem. Biophys.* **277**:374-381, 1990).

The small amounts of (-)-limonene and (-)-camphene formed by the recombinant enzyme are attributed to antipodal cyclizations via abnormal extended conformations, as the phenomenon has been described previously, especially when
25 using neryl diphosphate (the *cis*-analog of geranyl diphosphate) as an alternate substrate (Croteau et al., *J. Biol. Chem.* **263**:10063-10071, 1988; Croteau, R., and Satterwhite, D. M., *J. Biol. Chem.* **264**:15309-15315, 1989). The geranyl substrate, however, was verified as >99% pure, thereby eliminating this possibility in the present instance and suggesting that loss of stereochemical fidelity (to the extent of 5% of the
30 total product mixture) may be attributed to the presence of the glutathione-*S*-transferase fusion peptide plus transit peptide which may alter substrate binding directly, or indirectly by compromising subunit assembly.

Thus, the physical properties of the recombinant (+)-bornyl diphosphate synthase, together with the distribution and stereochemistry of its products, suggest
35 that this enzyme might represent both (+)-bornyl diphosphate synthase and (+)-pinene

-37-

synthase which were previously assumed to be distinct enzymes. The resolution of this question will require the detailed assessment of truncated enzymes that more closely resemble the native form, and which will therefore be likely to produce the same mixture of monoterpenes as the native form.

- 5 *Physical Properties of SCS and SSS.* Gel permeation chromatography of SCS revealed a single peak of activity at an elution volume corresponding to an M_r of 72,000, whereas SSS gave two peaks of activity, an aggregated form eluting in the void volume and a second corresponding to an M_r of 60,000. Both of these molecular weights are significantly lower than those predicted from pGEX
- 10 expression-based fusion of the glutathione-S-transferase (27 kDa) with the respective preproteins (SCS ~96 kDa and SSS ~96 kDa). Thrombin treatment was without influence on the gel permeation chromatographic behavior of these enzymes, indicating the absence of the glutathione-S-transferase peptide tag and rationalizing the previously observed inability of the recombinant SCS and SSS enzymes to bind to the
- 15 glutathione affinity column. Inspection of the 5'-sequences of the corresponding pGEX constructs showed both to be free of in-frame stop codons that might have permitted polycistronic translation of the preprotein devoid of the glutathione-S-transferase peptide. The apparent truncation was therefore attributed to proteolytic processing of the recombinant SCS and SSS in the *E. coli* host to proteins that
- 20 seemingly resemble the preprotein forms of the native, monomeric, sage 1,8-cineole synthase (Croteau et al., *Arch. Biochem. Biophys.* 309:184-192, 1994; Croteau, R., and Karp, F., *Arch. Biochem. Biophys.* 179:257-265, 1977) and (+)-sabinene synthase (Croteau, R., in *Recent Developments in Flavor and Fragrance Chemistry* (Hopp, R., and Mori, K., eds), pp. 263-273, VCH, Weinheim, Germany, 1992;
- 25 Croteau, R., in *Flavor Precursors: Thermal and Enzymatic Conversions* (Teranishi, R., Takeoka, G.R., and Guntert, M., eds), American Chemical Society Symposium Series, No. 490, pp. 8-20, Washington, DC, 1992). Similar proteolytic processing of a recombinant limonene synthase preprotein from spearmint has been observed previously in this *E. coli* host (Colby et al., *J. Biol. Chem.* 268:23016-23024, 1993).
- 30 1,8-Cineole synthase has never been satisfactorily separated from the aforementioned (-)-pinene synthase from sage but, in this instance, the product distribution of SCS does not match well the product distribution of (-)-pinene synthase either quantitatively, qualitatively, or in stereochemical terms, since the reactions catalyzed are of the opposite antipodal series (Croteau et al., *Arch.*
- 35 *Biochem. Biophys.* 309:184-192, 1994; Gambliel, H., and Croteau, R., *J. Biol. Chem.*

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257:2335-2342, 1982; Croteau et al., *J. Biol. Chem.* 264:2075-2080, 1989). However, the product distribution of SCS shows some parallels with that of the recently described cyclase III which produces (+)- α -pinene and (+)- β -pinene (Wagschal et al., *Arch. Biochem. Biophys.* 308:477-487, 1994; Pyun et al., *Arch. Biochem. Biophys.* 308:488-496, 1994). Even here, the match is not perfect and the production of anomalous products of the antipodal (-)-series (<6% of total) again suggests that substrate binding interactions may be compromised by the presence of the substantial transit peptide.

To assess the latter possibility, the K_m values for SCS (7.0 μ M), SSS (7.4 μ M) and SBS (3.0 μ M) were determined. These values are likely somewhat high because the recombinant enzymes were not purified sufficiently to remove all contaminating phosphatases that result in some depletion of the substrate geranyl diphosphate. While the calculated K_m values compare reasonably well with the literature values of 1.1 μ M (Croteau et al., *Arch. Biochem. Biophys.* 309:184-192, 1994), 2.0 μ M (Croteau, R., in *Recent Developments in Flavor and Fragrance Chemistry* (Hopp, R., and Mori, K., eds), pp. 263-273, VCH, Weinheim, Germany, 1992) and 2.0 μ M (Croteau et al., *J. Biol. Chem.* 264:2075-2080, 1989; Croteau et al., *Arch. Biochem. Biophys.* 277:374-381, 1990), respectively, for the corresponding native enzymes, they are sufficiently higher to suggest at least subtle alteration in binding capacity of the recombinant forms.

Example 7

Hybridization Conditions and Representative Sequences

The nucleic acid sequences of the present invention that encode at least a portion of a (+)-bornyl diphosphate synthase protein, or that are complementary to at least a portion of the nucleic acid sequence set forth in SEQ ID NO:1, are capable of hybridizing to the nucleic acid sequence set forth in SEQ ID NO:1, or to its complementary sequence, under the following conditions: 3x SSC at 65°C for 16 hours.

The nucleic acid sequences of the present invention that encode at least a portion of a (+)-bornyl diphosphate synthase protein, or that are complementary to at least a portion of the nucleic acid sequence set forth in SEQ ID NO:1, are capable of remaining hybridized to the nucleic acid sequence set forth in SEQ ID NO:1, or to its complementary sequence, under the following conditions: two washes (twenty minutes per wash) in 2x SSC at a temperature in the range of from 18°C to 24°C; preferably two washes (twenty minutes per wash) in 2x SSC at a temperature in the

range of from 18°C to 24°C, followed by one wash in 0.5x SSC for 30 minutes at 55°C; most preferably two washes (fifteen minutes per wash) in 2x SSC at a temperature in the range of from 18°C to 24°C, followed by two washes (twenty minutes per wash) in 0.2x SSC at a temperature of 65°C.

5 The nucleic acid sequences of the present invention that encode at least a portion of a (+)-sabinene synthase protein, or that are complementary to at least a portion of the nucleic acid sequence set forth in SEQ ID NO:5, are capable of hybridizing to the nucleic acid sequence set forth in SEQ ID NO:5, or to its complementary sequence, under the following conditions: 3x SSC at 65°C for 16
10 hours.

 The nucleic acid sequences of the present invention that encode at least a portion of a (+)-sabinene synthase protein, or that are complementary to at least a portion of the nucleic acid sequence set forth in SEQ ID NO:5, or to its complementary sequence, are capable of remaining hybridized to the nucleic acid
15 sequence set forth in SEQ ID NO:5, or to its complementary sequence, under the following conditions: two washes (twenty minutes per wash) in 2x SSC at a temperature in the range of from 18°C to 24°C; preferably two washes (twenty minutes per wash) in 2x SSC at a temperature in the range of from 18°C to 24°C, followed by one wash in 0.5x SSC for 30 minutes at 55°C; most preferably two
20 washes (fifteen minutes per wash) in 2x SSC at a temperature in the range of from 18°C to 24°C, followed by two washes (twenty minutes per wash) in 0.2x SSC at a temperature of 65°C.

 The nucleic acid sequences of the present invention that encode at least a portion of a 1,8-cineole synthase protein, or that are complementary to at least a
25 portion of the nucleic acid sequence set forth in SEQ ID NO:3, are capable of hybridizing to the nucleic acid sequence set forth in SEQ ID NO:3, or to its complementary sequence, under the following conditions: 3x SSC at 65°C for 16 hours.

 The nucleic acid sequences of the present invention that encode at least a
30 portion of a 1,8-cineole synthase protein, or that are complementary to at least a portion of the nucleic acid sequence set forth in SEQ ID NO:3, or to its complementary sequence, are capable of remaining hybridized to the nucleic acid sequence set forth in SEQ ID NO:3, or to its complementary sequence, under the following conditions: two washes (twenty minutes per wash) in 2x SSC at a
35 temperature in the range of from 18°C to 24°C; preferably two washes (twenty

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minutes per wash) in 2x SSC at a temperature in the range of from 18°C to 24°C, followed by one wash in 0.5x SSC for 30 minutes at 55°C; most preferably two washes (fifteen minutes per wash) in 2x SSC at a temperature in the range of from 18°C to 24°C, followed by two washes (twenty minutes per wash) in 0.2x SSC at a temperature of 65°C.

Representative nucleic acid sequences of the present invention that encode (+)-bornyl diphosphate synthase are set forth in SEQ ID NO:1, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32. Each of the foregoing, representative nucleic acid sequences encode the same (+)-bornyl diphosphate synthase protein sequence.

Representative (+)-bornyl diphosphate synthase proteins of the present invention are set forth in SEQ ID NO:2, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41 and SEQ ID NO:42.

Representative nucleic acid sequences of the present invention that encode (+)-sabinene synthase are set forth in SEQ ID NO:5, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59. Each of the foregoing, representative nucleic acid sequences encode the same (+)-sabinene synthase protein sequence.

Representative (+)-sabinene synthase proteins of the present invention are set forth in SEQ ID NO:6, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69.

Representative nucleic acid sequences of the present invention that encode 1,8-cineole synthase are set forth in SEQ ID NO:3, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84 and SEQ ID NO:86. Each of the foregoing, representative nucleic acid sequences encode the same 1,8 cineole synthase protein sequence.

Representative 1,8-cineole synthase proteins of the present invention are set forth in SEQ ID NO:4, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96 and SEQ ID NO:97.

It will be recognized that, based on the disclosure of the present application, one of ordinary skill in the art can readily identify and generate numerous amino acid

sequences and nucleic acid sequences that fall within the scope of the present invention. Thus, by way of non-limiting example, one of ordinary skill in the art will recognize that it is possible to make numerous, conservative amino acid substitutions in the protein sequences set forth, for example, in SEQ ID NO:2, SEQ ID NO:4 and
5 SEQ ID NO:6 which do not significantly adversely affect the enzymatic activity of the modified proteins. The term "conservative substitution" refers to substituting an amino acid with a side chain that is similar in charge and/or structure to that of the native molecule.

Further, one of ordinary skill in the art will recognize that, with the aid of a
10 genetic code table, it is possible to generate numerous nucleic acid sequences that encode any or all of the (+)-bornyl diphosphate synthase, 1,8-cineole synthase and (+)-sabinene synthase protein sequences disclosed herein.

While the preferred embodiment of the invention has been illustrated and described, it will be appreciated that various changes can be made therein without
15 departing from the spirit and scope of the invention.

The embodiments of the invention in which an exclusive property or privilege is claimed are defined as follows:

1. An isolated nucleic acid sequence encoding (+)-bornyl diphosphate synthase, 1,8-cineole synthase or (+)-sabinene synthase from an angiosperm plant species.
2. An isolated nucleic acid sequence of Claim 1 encoding (+)-bornyl diphosphate synthase.
3. An isolated nucleic acid sequence of Claim 2 encoding (+)-bornyl diphosphate synthase from an essential oil plant species.
4. An isolated nucleic acid sequence of Claim 3 encoding (+)-bornyl diphosphate synthase from *Salvia officinalis*.
5. An isolated nucleic acid sequence of Claim 4 consisting of the nucleic acid sequence set forth in SEQ ID NO:1.
6. An isolated nucleic acid sequence of Claim 1 encoding 1,8-cineole synthase.
7. An isolated nucleic acid sequence of Claim 6 encoding 1,8-cineole synthase from an essential oil plant species.
8. An isolated nucleic acid sequence of Claim 7 encoding 1,8-cineole synthase from *Salvia officinalis*.
9. An isolated nucleic acid sequence of Claim 8 consisting of the nucleic acid sequence set forth in SEQ ID NO:3.
10. An isolated nucleic acid sequence of Claim 1 encoding (+)-sabinene synthase.
11. An isolated nucleic acid sequence of Claim 10 encoding (+)-sabinene synthase from an essential oil plant species.

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12. An isolated nucleic acid sequence of Claim 11 encoding (+)-sabinene synthase from *Salvia officinalis*.

13. An isolated nucleic acid sequence of Claim 12 consisting of the nucleic acid sequence set forth in SEQ ID NO:5.

14. A replicable expression vector comprising a nucleic acid sequence encoding (+)-bornyl diphosphate synthase, 1,8-cineole synthase or (+)-sabinene synthase from an angiosperm plant species.

15. A replicable expression vector of Claim 14 wherein the nucleotide sequence comprises the sequence of SEQ ID NO:1, SEQ ID NO:3 or SEQ ID NO:5.

16. A host cell comprising a vector of Claim 14 or Claim 15.

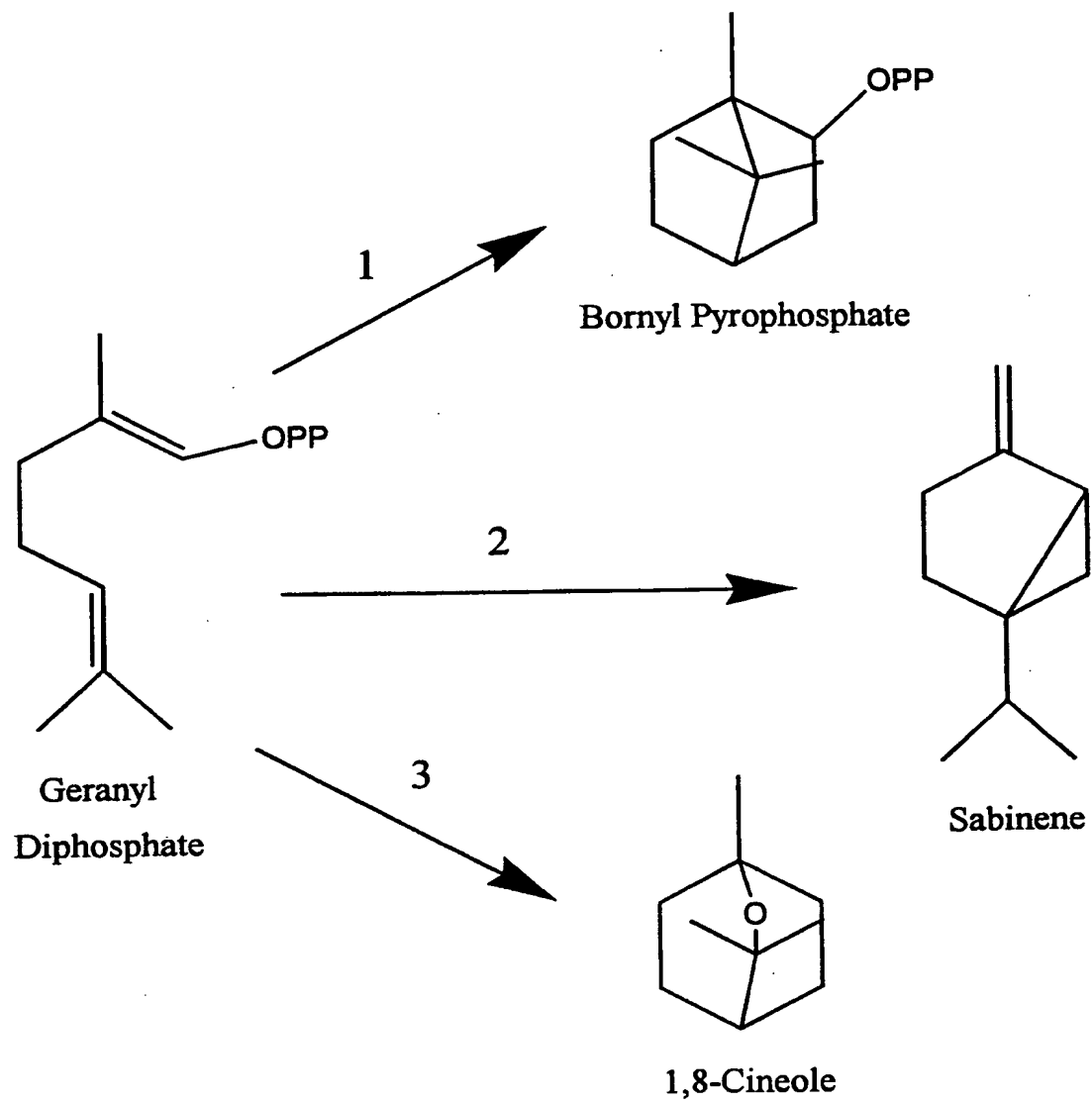
17. A method of altering the expression of (+)-bornyl diphosphate synthase in a suitable host cell comprising introducing into the host cell an expression vector that comprises a nucleotide sequence encoding an angiosperm (+)-bornyl diphosphate synthase protein under conditions enabling expression of the protein in the host cell.

18. A method of altering the expression of 1,8-cineole synthase in a suitable host cell comprising introducing into the host cell an expression vector that comprises a nucleotide sequence encoding an angiosperm 1,8-cineole synthase protein under conditions enabling expression of the protein in the host cell.

19. A method of altering the expression of (+)-sabinene synthase in a suitable host cell comprising introducing into the host cell an expression vector that comprises a nucleotide sequence encoding an angiosperm (+)-sabinene synthase protein under conditions enabling expression of the protein in the host cell.

20. An isolated nucleic acid sequence that hybridizes, in a solution comprising 3x SSC at a temperature of 65°C, to any one of the nucleic acid sequences set forth in SEQ ID NO:1, SEQ ID NO:3 and SEQ ID NO:5, said isolated nucleic acid sequence remaining hybridized to any one of the nucleic acid sequences set forth in SEQ ID NO:1, SEQ ID NO:3 and SEQ ID NO:5 in a solution comprising 0.5x SSC at a temperature of 55°C.

1/1

**FIGURE 1**

SEQUENCE LISTING

<110> Croteau, Rodney B
 Wise, Mitchell L
 Savage, Thomas J
 Katahira, Eva J

<120> Monoterpene Synthases from Common Sage (*Salvia officinalis*)

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 Pro Leu Asn Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu
 15 20 25

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 80 85 90

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 Arg Ile Leu Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu
 95 100 105

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ctg cag aaa aaa ctt gat gaa ggt ggt aat gaa att gat gag aat cta Leu Gln Lys Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu 225 230 235	721
tta ttg tgg att cgc cac tct ttg gat ctt cct ctc cac tgg agg att Leu Leu Trp Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile 240 245 250	769
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 590 595

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Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu Leu Val Pro
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Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser Ser Lys Leu
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Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln Pro Ala Leu
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Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Thr Glu Glu
 65 70 75 80

Arg His Leu Asp Arg Lys Ala Glu Leu Ile Val Gln Val Arg Ile Leu
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Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu Ile His Asp
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Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu Ile Lys Glu
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Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His Asn Asn Glu
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Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Leu Leu
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Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn Cys Phe Lys
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Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln Asp Thr Lys
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Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Lys Gly Glu
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Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys Leu Gln Lys
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Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu Leu Leu Trp
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 Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile Gln Ser Val
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 Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn
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 Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu
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 Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser
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 Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln
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 Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp
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Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly
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 Pro Ala Lys Ile Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg
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 Cys Ser Leu Gln Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly
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 Gly Tyr Gln Pro Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp
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 Ser Glu Tyr Lys Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile
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 Leu Glu Leu Ile Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe
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 gac cgc gag atc gtt gaa ata tta aac tca aaa tat tat acc aac aat 433
 Asp Arg Glu Ile Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn
 125 130 135 140

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 Thr Leu Arg Asp Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala
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 Trp Val Asp Leu Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr
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 Thr Ser Leu Asp Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln
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 Cys Tyr Met Asn Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His
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 Met Thr Ser Ser Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu
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gca aga atg gcg caa tgg ata tac cag cat gaa tct gat gga ttt ggc 1729
 Ala Arg Met Ala Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly
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 Met Gln His Ser Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp
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cgc tat gag taactaatct tcgcccgggt tccaaatgaa tcaatctgtt 1826
 Arg Tyr Glu
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gtgttgctgt tccacctgat atcaataata attagacaaa tgtttctgta cgggtggccc 1886

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1968

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 Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro
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 Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser Glu Tyr Lys
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 Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala Gln Val Asn
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 Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu Ile Asp Glu
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 Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr
 145 150 155 160
 Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys
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 Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg Gly Leu Leu
 180 185 190
 Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu Glu Thr Leu
 195 200 205
 His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys Arg Val Leu
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 225 230 235 240
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 245 250 255
 Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val Leu Glu Leu
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Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln Gln Glu Leu
 275 280 285
 Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val His Glu Leu
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 Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp Thr Thr Gly
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 Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met Leu Thr Lys
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 Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp
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Phe	Asp	Glu	Gly	Gly	Asp	Glu	Ile	Asp	Glu	Asp	Leu	Ser	Ser	Trp	Ile		
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cgc	cat	tcc	ttg	gat	ctt	cct	ctt	cat	tgg	agg	gtc	caa	gga	tta	gag	771	
Arg	His	Ser	Leu	Asp	Leu	Pro	Leu	His	Trp	Arg	Val	Gln	Gly	Leu	Glu		
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gca	aga	tgg	ttc	tta	gat	gct	tat	gcg	agg	agg	ccg	gac	atg	aat	cca	819	
Ala	Arg	Trp	Phe	Leu	Asp	Ala	Tyr	Ala	Arg	Arg	Pro	Asp	Met	Asn	Pro		
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Tyr	Gln	Glu	Glu	Leu	Lys	Asp	Ile	Ser	Arg	Trp	Trp	Asn	Ser	Ser	Cys		
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Tyr	Asp	Val	Tyr	Gly	Thr	Ile	Glu	Glu	Leu	Glu	Leu	Leu	Thr	Asp	Met		
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Gln	Val	Cys	Tyr	Leu	Ala	Leu	Tyr	Asn	Phe	Val	Ser	Glu	Arg	Ala	Tyr		
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Ser	Trp	Val	Ser	Leu	Val	Glu	Gly	Tyr	Leu	Lys	Glu	Ala	Tyr	Trp	Tyr		
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      445              450              455
gca aac tcg att gat gaa aca gct atc gag agc ttg tac caa tat cat 1443
Ala Asn Ser Ile Asp Glu Thr Ala Ile Glu Ser Leu Tyr Gln Tyr His
      460              465              470
aac ata ctt tac cta tca gga acc ata tta agg ctt gct gac gat ctt 1491
Asn Ile Leu Tyr Leu Ser Gly Thr Ile Leu Arg Leu Ala Asp Asp Leu
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ggg aca tca caa cat gag ctg gag aga gga gac gta ccg aaa gca atc 1539
Gly Thr Ser Gln His Glu Leu Glu Arg Gly Asp Val Pro Lys Ala Ile
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cag tgc tac atg aat gac aca aat gct tcg gag aga gag gcg gtg gaa 1587
Gln Cys Tyr Met Asn Asp Thr Asn Ala Ser Glu Arg Glu Ala Val Glu
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cac gtg aag ttt ctg ata agg gag gcg tgg aag gag atg aac acg gtc 1635
His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Glu Met Asn Thr Val
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Thr Thr Ala Ser Asp Cys Pro Phe Thr Asp Asp Leu Val Ala Ala Ala
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Ala Asn Leu Ala Arg Ala Ala Gln Phe Ile Tyr Leu Asp Gly Asp Gly
      555              560              565
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His Gly Val Gln His Ser Glu Ile His Gln Gln Met Gly Gly Leu Leu
      570              575              580              585
ttc cag cct tat gtctgaataa atcgaaaatc caacctacta tgtatccctc 1831
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Gly	Tyr	Leu	Lys	Glu	Ala	Tyr	Trp	Tyr	Tyr	Asn	Gly	Tyr	Lys	Pro	Ser
			420					425					430		
Leu	Glu	Glu	Tyr	Leu	Asn	Asn	Ala	Lys	Ile	Ser	Ile	Ser	Ala	Pro	Thr
		435					440					445			
Ile	Ile	Ser	Gln	Leu	Tyr	Phe	Thr	Leu	Ala	Asn	Ser	Ile	Asp	Glu	Thr
450					455					460					
Ala	Ile	Glu	Ser	Leu	Tyr	Gln	Tyr	His	Asn	Ile	Leu	Tyr	Leu	Ser	Gly
465				470					475						480
Thr	Ile	Leu	Arg	Leu	Ala	Asp	Asp	Leu	Gly	Thr	Ser	Gln	His	Glu	Leu
				485					490					495	
Glu	Arg	Gly	Asp	Val	Pro	Lys	Ala	Ile	Gln	Cys	Tyr	Met	Asn	Asp	Thr
			500					505					510		
Asn	Ala	Ser	Glu	Arg	Glu	Ala	Val	Glu	His	Val	Lys	Phe	Leu	Ile	Arg
		515					520					525			
Glu	Ala	Trp	Lys	Glu	Met	Asn	Thr	Val	Thr	Thr	Ala	Ser	Asp	Cys	Pro
		530				535					540				
Phe	Thr	Asp	Asp	Leu	Val	Ala	Ala	Ala	Ala	Asn	Leu	Ala	Arg	Ala	Ala
545				550					555						560
Gln	Phe	Ile	Tyr	Leu	Asp	Gly	Asp	Gly	His	Gly	Val	Gln	His	Ser	Glu
				565				570						575	
Ile	His	Gln	Gln	Met	Gly	Gly	Leu	Leu	Phe	Gln	Pro	Tyr			
			580				585								

<210> 7
 <211> 2022
 <212> DNA
 <213> *Salvia officinalis*

<400> 7
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 gaatgcaaat ggcgttttct agcaacccaa ttaaacaatc tcataactca gacatcaagt 120
 cttcaaaaact aatttccagt aatagaattg gtagcagtga tgctgctcgc ctccgcctgc 180
 attgctcctc gcagcaacac ggtgccgatg agctccaaac gcaccgacga tctggaaaact 240
 acagtccttc ccgatgggat ttcgattata ttcaatcact ccacagtgat tataaggaag 300

aaagacacag aagaagggct agtgagctag ttatgcaagt gaagaagcta atagagaaag 360
 aaacggatcc cactcgacag ttggagctaa tggatgactt gcagaggctg ggcctgggtg 420
 atcatttcca ggatgaattc aaggaaatct taatctctgt atatttgac aataaatatt 480
 acaagagtaa tgtggataat atgaaaaagg ccgaaagga tttgtactcg acggctcttg 540
 cattcagact ccttagacaa catggttttc atgttgcctc agagggtgtg ggggtgttca 600
 agaacgatga gggcgacttc gaaccaagcc ttgtccatga caccagagga ttgctgcaac 660
 tgtacgaagc ttccttcttg ctgacacaag gcgaaaacac actcgagtta gctagagaat 720
 ttgcctccag aattctgcag gagaaactac tgaatgatga gattgatgac attaaccttt 780
 cgacatggat actcaattct ttggacatcc caatccattg gaggattgaa aggggtgaaca 840
 caagtgtgtg gatagaagca tacaagaggc gagccgacat gaatccaaca gtgctggatc 900
 ttgccatact ggacaccaat attgtacaag cacagtatca ggaggaaactc aaacagaact 960
 tacagtgggtg gagaaattca ggaattgtgg agaagcttcc cttcgtgagg aacaggctag 1020
 tggagtccca cttttggagc gttgggatcg tgcagcctcg tcaacatgga attggaagaa 1080
 tggcattggg caaatccatc gctcttataa caaccataaa tgatgtttat gatgtgtatg 1140
 gtacattaga agaactcgaa caattcacag acgtcattcg aagatgggat ataagttcaa 1200
 tagacaaact ccctagctat atgcaactgt gttttcttgc actgcacaac tttgtgaacg 1260
 atacggccta tgatgtgcta aaagagcaag gtttcaacat catcccatat ctccgaaaat 1320
 cgtggatgga tttggtggag gcatatctgg tggaggccaa gtggtaccac agtggataca 1380
 aaccaaactc ggaagagtat ttggagaact catggatctc agactcaggc cctgctgtac 1440
 tagcccaagc atttttcggc gtaacacatt ctcttacaga ggaggccgc cactgtttgt 1500
 acggacacca cgatttaatt cgttcgtcat caatgatttt gcgacttgct gatgatctag 1560
 gaacctcttc ggaatgggcc atgtgaaacg ggacagtcca atttggaaag tgggccatgt 1620
 gaaacgagac ggagggagta atacatcaac aaatcaacac ttgcttcttc caccctgcaa 1680
 cactctagct acgtacctat gtatatatta tatatgcata tgcattgctt gcacacatta 1740
 atcaaggaat aatcaatgca tcacatata tatctacttc tattttatat gttctacttc 1800
 taacctttcg tttagtatca tttaaattttc ttttatttta tatattatgt tttgaattga 1860
 agctgttttt actgtcttta attcactata aacaaatatt gcgtatattt tcgagaatgg 1920
 aattaataac atgatttttg agaaaaaaaa tgaaattatg taggaattaa agataaaatt 1980
 tgaaaaaaaa aaaaaaaaaa ctcgaggggg gcccgtacc aa 2022

<210> 8
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer 1F

<220>

<221> misc_feature

<222> (1)..(26)

<223> PCR primer 1F where "N" is inosine

<400> 8

aaraaygarr arggnganta yaarga

26

<210> 9
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer 2F

<220>

<221> misc_feature

<222> (1)..(17)

<223> PCR primer 2F where "N" is inosine

<400> 9

ytncarytnt aygargc

17

<210> 10
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer 3R

<220>

<221> misc_feature

<222> (1)..(24)

<223> PCR primer 3R where "N" is inosine

<400> 10

ctrgtyrang gnmtratrta cgty

24

<210> 11
 <211> 659
 <212> DNA
 <213> Salvia officinalis

<400> 11

ttgcatgcct gcaggctgac tctagaggat ctactagtca tatggattgg tctagattgc 60

atgtaatcgg ggaggttgtc gattgaactc atatcccatc ttcgaatgac gtctgtgaat 120

tgttccagtt cttccaaagt accatacaca tcgtaaacat catctatcgt gggtataaga 180
 gcattcactt tgcccaccgt tacccttgca ttgcatgct gacgaggctg cagcatccca 240
 gtagtccaga agtagcattc cacaagtcgg tccctcgcga aggggagctt ctccacgatg 300
 cagctacttc tccaccactg taagtcctgt ttgagttcct cttgatattg tgettgtaca 360
 atattcgagt ccagtatggc aagctccaac acgatggatt catgtcggat ctctcttat 420
 aggcacgat ccacgtgctt gcatttcctc ttccaatcct ccaatggatt gggatgtcca 480
 aagcatagcg tatcgacaat aaaaggtaaa ggtcttcgtt actttcctcc ttcagtttgt 540
 cctcaaggat tttggcggcg aactccctgc ctaaatccag cgtcttctca ccttccatcg 600
 tcaaaaacga agcttcgtac aattgcagca taatcggatc cccgggtaccg agctcgaan 659

<210> 12

<211> 584

<212> DNA

<213> *Salvia officinalis*

<400> 12

ggtctagact tcatgtagtc ggggaggttg tctattgaac ttatatccca tcttcgaatg 60
 acgtctgtga actgttcgag ttcttctaatt gtaccataca catcataaac atcatattatg 120
 gttgttataa gagcgatgga tttgcccaat gccattcttc caattccatg ttgacgaggc 180
 tgcaegatcc caacgtccca aaagtaggac tccactagcc tgttcctcac gaagggaagc 240
 ttctccacaa ttcctgaatt tctccaccac tgtaagttct gtttgagttc ctctgatac 300
 tgtgcttgta caatattggt gtccagtatg gcaagatcca gcaactgttg attcatgtcg 360
 gctgcctct tgtatgcttc tatccacaca cttgtgttca ccttttcaat cctccaatgg 420
 attgggatgt ccaaagaatt gagtatccat gtcgaaaggt taatgtcatc aatctcatca 480
 ttcagtagtt tctcctgcag aattctggag gcaaattctc tagctaactc gagtgtgttt 540
 tcgccttggt tcagcaagaa ggaagcctcg tacaactgca gcat 584

<210> 13

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: conserved amino acid sequence

<220>

<221> DOMAIN

<222> (1)..(6)

<223> Conserved sequence found in all

prenyltransferases. Xaa at position 1 is I, L or V. Xaa at positions 4 and 5 represent any amino acid

<400> 13

Xaa Asp Asp Xaa Xaa Asp
1 5

<210> 14

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: conserved sequence

<220>

<221> DOMAIN

<222> (1)..(5)

<223> Conserved prenyltransferase sequence. Xaa at position 4 represents any amino acid. Xaa at position 5 represents Glu or Asp

<400> 14

Cys Tyr Met Xaa Xaa
1 5

<210> 15

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: active site peptide

<220>

<221> DOMAIN

<222> (1)..(10)

<223> Monoterpene synthase active site peptide

<400> 15

Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu
1 5 10

<210> 16

<211> 2024

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
computer-generated nucleic acid encoding
(+)-bornyl diphosphate synthase

<220>

<221> CDS

<222> (11)..(1804)

<400> 16

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gatcacaaaa atg tct atc att agc atg aac gta tcg atc ctt agc aag      49
      Met Ser Ile Ile Ser Met Asn Val Ser Ile Leu Ser Lys
            1              5              10

cca cta aat tgc ctc cac aac ttg gag agg aga cct tca aaa gcc ttg      97
Pro Leu Asn Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu
      15              20              25

ctt gtc cct tgc act gca ccc acc gct cgc ctc cgg gca tct tgc tcc      145
Leu Val Pro Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser
      30              35              40              45

tca aaa cta caa gaa gct cat caa atc cga cga tct gga aac tac caa      193
Ser Lys Leu Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln
              50              55              60

cct gcc att tgg gat tcc aat tac att cag tct ctc aat act cca tat      241
Pro Ala Ile Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr
              65              70              75

acg gag gag agg cac ttg gat aga aaa gca gag ctg att gtg caa gtg      289
Thr Glu Glu Arg His Leu Asp Arg Lys Ala Glu Leu Ile Val Gln Val
      80              85              90

agg ata ctg cta aag gaa aaa atg gag cct gtt caa caa ttg gag ttg      337
Arg Ile Leu Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu
      95              100              105

att cat gac ttg aaa tat ttg ggg ctc tcg gat ttt ttt caa gat gag      385
Ile His Asp Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu
      110              115              120              125

att aag gag atc tta ggt gtt ata tac aat gag cac aaa tgc ttt cac      433
Ile Lys Glu Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His
              130              135              140

aat aat gaa gta gag aaa atg gat ttg tat ttc aca gct ctt gga ttc      481
Asn Asn Glu Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe
              145              150              155

aga ctc ctc aga caa cat ggt ttt aat att tcc caa gat gta ttt aat      529
Arg Leu Leu Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn
              160              165              170

tgt ttc aag aac gag aag ggt att gat ttc aag gca agc ctt gct caa      577
Cys Phe Lys Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln
      175              180              185

gat acg aag gga atg tta caa ctg tat gaa gcg tct ttc ctt ttg aga      625
Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg
      190              195              200              205

aaa ggt gaa gat aca ttg gag ctt gca aga gaa ttt gcc aca aaa tgt      673
Lys Gly Glu Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys
              210              215              220

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ctg cag aaa aaa ctt gat gaa ggt ggt aat gaa att gat gag aat cta Leu Gln Lys Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu 225 230 235	721
tta ttg tgg att cgc cac tct ttg gat ctt cct ctc cac tgg agg att Leu Leu Trp Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile 240 245 250	769
caa agt gta gag gca aga tgg ttc ata gat gct tat gcg aga agg cca Gln Ser Val Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro 255 260 265	817
gac atg aat cca ctt att ttc gag ctt gcc aaa ctc aac ttc aat att Asp Met Asn Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile 270 275 280 285	865
att caa gca aca cat caa caa gaa ctg aaa gat ctc tcg agg tgg tgg Ile Gln Ala Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp 290 295 300	913
agt aga tta tgc ttc cct gaa aag ctc cca ttt gtg agg gat agg ctc Ser Arg Leu Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu 305 310 315	961
gtt gaa tcc ttc ttt tgg gcg gtt ggg atg ttt gag cca cat caa cat Val Glu Ser Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His 320 325 330	1009
gga tat cag aga aaa atg gcc gcc aca att att gtt tta gca aca gtt Gly Tyr Gln Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val 335 340 345	1057
ata gat gat att tac gat gtg tat ggt aca cta gat gaa cta gaa cta Ile Asp Asp Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu 350 355 360 365	1105
ttt aca gac acg ttt aag aga tgg gat act gaa tca ata acc cga ctt Phe Thr Asp Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu 370 375 380	1153
cct tat tac atg caa tta tgt tat tgg ggt gtc cac aac tat att tcc Pro Tyr Tyr Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser 385 390 395	1201
gat gca gca tat gat att ctc aaa gaa cat ggt ttc ttt tgt ctc caa Asp Ala Ala Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln 400 405 410	1249
tat ctc cgg aaa tcg gtg gta gat ttg gtt gaa gca tat ttt cac gag Tyr Leu Arg Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu 415 420 425	1297
gca aag tgg tac cac agc ggt tat aca cca agc ctg gat gaa tat ctc Ala Lys Trp Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu 430 435 440 445	1345
aac atc gcc aag att tca gtg gcg tct cct gca ata ata tcc cca acc Asn Ile Ala Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr 450 455 460	1393

tat ttc aca ttc gca aac gcg tct cat gac aca gca gtc atc gac agc 1441
 Tyr Phe Thr Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser
 465 470 475
 ttg tac caa tat cat gac ata ctt tgc cta gca gga att att ttg agg 1489
 Leu Tyr Gln Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg
 480 485 490
 ctt ccc gac gat ctt ggg aca tca tat ttt gag ctg gcg aga ggc gac 1537
 Leu Pro Asp Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp
 495 500 505
 gtg ccg aaa aca atc cag tgc tac atg aag gaa aca aat gct agt gag 1585
 Val Pro Lys Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu
 510 515 520 525
 gag gag gcg gtg gag cac gtg aag ttt ctg ata agg gag gcg tgg aag 1633
 Glu Glu Ala Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys
 530 535 540
 gat atg aac acg gcc ata gca gcc ggt tat ccg ttt ccg gat ggt atg 1681
 Asp Met Asn Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met
 545 550 555
 gtg gcg ggc gca gct aat att ggg cgc gtg gcg cag ttt att tat ctc 1729
 Val Ala Gly Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu
 560 565 570
 cac gga gat ggg ttt ggc gtg caa cac tcg aaa acg tac gag cat atc 1777
 His Gly Asp Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile
 575 580 585
 gcc ggc cta ctg ttc gag cct tat gca tgaacaaatg ggagactgct 1824
 Ala Gly Leu Leu Phe Glu Pro Tyr Ala
 590 595
 tgatatatat taatttggca caccaataat tgcattgttat atatgttgga aaataagtgt 1884
 ctgggttgaga tgtcatgtgg tgtattatct aaataattca aggttgccctt gtttatgtag 1944
 ccggtggtgc aactacctcc cattcaaadc aattaaatct aaacagtcga gtcaagctcg 2004
 agctcgagga aaaaaaaaaa 2024

<210> 17

<211> 598

<212> PRT

<213> Artificial Sequence

<400> 17

Met Ser Ile Ile Ser Met Asn Val Ser Ile Leu Ser Lys Pro Leu Asn
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 Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu Leu Val Pro
 20 25 30
 Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser Ser Lys Leu
 35 40 45

Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln Pro Ala Ile
 50 55 60
 Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Thr Glu Glu
 65 70 75 80
 Arg His Leu Asp Arg Lys Ala Glu Leu Ile Val Gln Val Arg Ile Leu
 85 90 95
 Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu Ile His Asp
 100 105 110
 Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu Ile Lys Glu
 115 120 125
 Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His Asn Asn Glu
 130 135 140
 Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Leu Leu
 145 150 155 160
 Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn Cys Phe Lys
 165 170 175
 Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln Asp Thr Lys
 180 185 190
 Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Lys Gly Glu
 195 200 205
 Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys Leu Gln Lys
 210 215 220
 Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu Leu Leu Trp
 225 230 235 240
 Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile Gln Ser Val
 245 250 255
 Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn
 260 265 270
 Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile Ile Gln Ala
 275 280 285
 Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu
 290 295 300
 Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser
 305 310 315 320
 Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln
 325 330 335
 Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp
 340 345 350
 Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu Phe Thr Asp
 355 360 365

Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu Pro Tyr Tyr
 370 375 380
 Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser Asp Ala Ala
 385 390 395 400
 Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln Tyr Leu Arg
 405 410 415
 Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu Ala Lys Trp
 420 425 430
 Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu Asn Ile Ala
 435 440 445
 Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr Tyr Phe Thr
 450 455 460
 Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser Leu Tyr Gln
 465 470 475 480
 Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg Leu Pro Asp
 485 490 495
 Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp Val Pro Lys
 500 505 510
 Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu Glu Glu Ala
 515 520 525
 Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Asp Met Asn
 530 535 540
 Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly
 545 550 555 560
 Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu His Gly Asp
 565 570 575
 Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile Ala Gly Leu
 580 585 590
 Leu Phe Glu Pro Tyr Ala
 595

<210> 18

<211> 2024

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 computer-generated nucleic acid encoding
 (+)-bornyl diphosphate synthase

<220>

<221> CDS

<222> (11)..(1804)

<400> 18
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Met Ser Ile Ile Ser Met Asn Val Ser Ile Leu Ser Lys
1 5 10

cca cta aat tgc ctc cac aac ttg gag agg aga cct tca aaa gcc ttg 97
Pro Leu Asn Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu
15 20 25

ctt gtc cct tgc act gca ccc acc gct cgc ctc cgg gca tct tgc tcc 145
Leu Val Pro Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser
30 35 40 45

tca aaa cta caa gaa gct cat caa atc cga cga tct gga aac tac caa 193
Ser Lys Leu Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln
50 55 60

cct gcc ctt tgg gat tcc aat tac ctt cag tct ctc aat act cca tat 241
Pro Ala Leu Trp Asp Ser Asn Tyr Leu Gln Ser Leu Asn Thr Pro Tyr
65 70 75

acg gag gag agg cac ttg gat aga aaa gca gag ctg att gtg caa gtg 289
Thr Glu Glu Arg His Leu Asp Arg Lys Ala Glu Leu Ile Val Gln Val
80 85 90

agg ata ctg cta aag gaa aaa atg gag cct gtt caa caa ttg gag ttg 337
Arg Ile Leu Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu
95 100 105

att cat gac ttg aaa tat ttg ggg ctc tcg gat ttt ttt caa gat gag 385
Ile His Asp Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu
110 115 120 125

att aag gag atc tta ggt gtt ata tac aat gag cac aaa tgc ttt cac 433
Ile Lys Glu Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His
130 135 140

aat aat gaa gta gag aaa atg gat ttg tat ttc aca gct ctt gga ttc 481
Asn Asn Glu Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe
145 150 155

aga ctc ctc aga caa cat ggt ttt aat att tcc caa gat gta ttt aat 529
Arg Leu Leu Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn
160 165 170

tgt ttc aag aac gag aag ggt att gat ttc aag gca agc ctt gct caa 577
Cys Phe Lys Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln
175 180 185

gat acg aag gga atg tta caa ctg tat gaa gcg tct ttc ctt ttg aga 625
Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg
190 195 200 205

aaa ggt gaa gat aca ttg gag ctt gca aga gaa ttt gcc aca aaa tgt 673
Lys Gly Glu Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys
210 215 220

ctg cag aaa aaa ctt gat gaa ggt ggt aat gaa att gat gag aat cta 721
Leu Gln Lys Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu
225 230 235

tta ttg tgg att cgc cac tct ttg gat ctt cct ctc cac tgg agg att Leu Leu Trp Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile 240 245 250	769
caa agt gta gag gca aga tgg ttc ata gat gct tat gcg aga agg cca Gln Ser Val Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro 255 260 265	817
gac atg aat cca ctt att ttc gag ctt gcc aaa ctc aac ttc aat att Asp Met Asn Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile 270 275 280 285	865
att caa gca aca cat caa caa gaa ctg aaa gat ctc tcg agg tgg tgg Ile Gln Ala Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp 290 295 300	913
agt aga tta tgc ttc cct gaa aag ctc cca ttt gtg agg gat agg ctc Ser Arg Leu Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu 305 310 315	961
gtt gaa tcc ttc ttt tgg gcg gtt ggg atg ttt gag cca cat caa cat Val Glu Ser Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His 320 325 330	1009
gga tat cag aga aaa atg gcc gcc aca att att gtt tta gca aca gtt Gly Tyr Gln Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val 335 340 345	1057
ata gat gat att tac gat gtg tat ggt aca cta gat gaa cta gaa cta Ile Asp Asp Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu 350 355 360 365	1105
ttt aca gac acg ttt aag aga tgg gat act gaa tca ata acc cga ctt Phe Thr Asp Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu 370 375 380	1153
cct tat tac atg caa tta tgt tat tgg ggt gtc cac aac tat att tcc Pro Tyr Tyr Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser 385 390 395	1201
gat gca gca tat gat att ctc aaa gaa cat ggt ttc ttt tgt ctc caa Asp Ala Ala Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln 400 405 410	1249
tat ctc cgg aaa tcg gtg gta gat ttg gtt gaa gca tat ttt cac gag Tyr Leu Arg Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu 415 420 425	1297
gca aag tgg tac cac agc ggt tat aca cca agc ctg gat gaa tat ctc Ala Lys Trp Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu 430 435 440 445	1345
aac atc gcc aag att tca gtg gcg tct cct gca ata ata tcc cca acc Asn Ile Ala Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr 450 455 460	1393
tat ttc aca ttc gca aac gcg tct cat gac aca gca gtc atc gac agc Tyr Phe Thr Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser 465 470 475	1441

ttg tac caa tat cat gac ata ctt tgc cta gca gga att att ttg agg 1489
 Leu Tyr Gln Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg
 480 485 490
 ctt ccc gac gat ctt ggg aca tca tat ttt gag ctg gcg aga ggc gac 1537
 Leu Pro Asp Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp
 495 500 505
 gtg ccg aaa aca atc cag tgc tac atg aag gaa aca aat gct agt gag 1585
 Val Pro Lys Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu
 510 515 520 525
 gag gag gcg gtg gag cac gtg aag ttt ctg ata agg gag gcg tgg aag 1633
 Glu Glu Ala Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys
 530 535 540
 gat atg aac acg gcc ata gca gcc ggt tat ccg ttt ccg gat ggt atg 1681
 Asp Met Asn Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met
 545 550 555
 gtg gcg ggc gca gct aat att ggg cgc gtg gcg cag ttt att tat ctg 1729
 Val Ala Gly Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu
 560 565 570
 cac gga gat ggg ttt ggc gtg caa cac tcg aaa acg tac gag cat atc 1777
 His Gly Asp Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile
 575 580 585
 gcc ggc cta ctg ttc gag cct tat gca tgaacaaatg ggagactgct 1824
 Ala Gly Leu Leu Phe Glu Pro Tyr Ala
 590 595
 tgatatatat taatttggca caccaataat tgcattgttat atatgttgga aaataagtgt 1884
 ctgggtgaga tgtcatgtgg tgtattatct aaataattca aggttgccctt gtttatgtag 1944
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 <211> 598
 <212> PRT
 <213> Artificial Sequence

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 Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser Ser Lys Leu
 35 40 45
 Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln Pro Ala Leu
 50 55 60

Trp Asp Ser Asn Tyr Leu Gln Ser Leu Asn Thr Pro Tyr Thr Glu Glu
 65 70 75 80
 Arg His Leu Asp Arg Lys Ala Glu Leu Ile Val Gln Val Arg Ile Leu
 85 90 95
 Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu Ile His Asp
 100 105 110
 Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu Ile Lys Glu
 115 120 125
 Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His Asn Asn Glu
 130 135 140
 Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Leu Leu
 145 150 155 160
 Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn Cys Phe Lys
 165 170 175
 Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln Asp Thr Lys
 180 185 190
 Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Lys Gly Glu
 195 200 205
 Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys Leu Gln Lys
 210 215 220
 Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu Leu Leu Trp
 225 230 235 240
 Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile Gln Ser Val
 245 250 255
 Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn
 260 265 270
 Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile Ile Gln Ala
 275 280 285
 Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu
 290 295 300
 Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser
 305 310 315 320
 Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln
 325 330 335
 Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp
 340 345 350
 Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu Phe Thr Asp
 355 360 365
 Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu Pro Tyr Tyr
 370 375 380

Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser Asp Ala Ala
 385 390 395 400
 Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln Tyr Leu Arg
 405 410 415
 Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu Ala Lys Trp
 420 425 430
 Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu Asn Ile Ala
 435 440 445
 Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr Tyr Phe Thr
 450 455 460
 Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser Leu Tyr Gln
 465 470 475 480
 Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg Leu Pro Asp
 485 490 495
 Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp Val Pro Lys
 500 505 510
 Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu Glu Glu Ala
 515 520 525
 Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Asp Met Asn
 530 535 540
 Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly
 545 550 555 560
 Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu His Gly Asp
 565 570 575
 Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile Ala Gly Leu
 580 585 590
 Leu Phe Glu Pro Tyr Ala
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<210> 20
 <211> 2024
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 computer-generated nucleic acid sequence encoding
 (+)-bornyl diphosphate synthase

<220>
 <221> CDS
 <222> (11)..(1804)

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Pro	Leu	Asn	Cys	Leu	His	Asn	Leu	Glu	Arg	Arg	Pro	Ser	Lys	Ala	Leu					
15						20					25									
ctt	gtc	cct	tgc	act	gca	ccc	acc	gct	cgc	ctc	cgg	gca	tct	tgc	tcc	145				
Leu	Val	Pro	Cys	Thr	Ala	Pro	Thr	Ala	Arg	Leu	Arg	Ala	Ser	Cys	Ser					
30				35					40				45							
tca	aaa	cta	caa	gaa	gct	cat	caa	atc	cga	cga	tct	gga	aac	tac	caa	193				
Ser	Lys	Leu	Gln	Ala	His	Gln	Ile	Arg	Arg	Ser	Gly	Asn	Tyr	Gln						
				50					55				60							
cct	gcc	ctt	tgg	gat	tcc	aat	tac	att	cag	tct	atc	aat	act	cca	tat	241				
Pro	Ala	Leu	Trp	Asp	Ser	Asn	Tyr	Ile	Gln	Ser	Ile	Asn	Thr	Pro	Tyr					
				65					70				75							
acg	gag	gag	agg	cac	ttg	gat	aga	aaa	gca	gag	ctg	att	gtg	caa	gtg	289				
Thr	Glu	Glu	Arg	His	Leu	Asp	Arg	Lys	Ala	Glu	Leu	Ile	Val	Gln	Val					
80				85					90											
agg	ata	ctg	cta	aag	gaa	aaa	atg	gag	cct	gtt	caa	caa	ttg	gag	ttg	337				
Arg	Ile	Leu	Leu	Lys	Glu	Lys	Met	Glu	Pro	Val	Gln	Gln	Leu	Glu	Leu					
95				100					105											
att	cat	gac	ttg	aaa	tat	ttg	ggg	ctc	tcg	gat	ttt	ttt	caa	gat	gag	385				
Ile	His	Asp	Leu	Lys	Tyr	Leu	Gly	Leu	Ser	Asp	Phe	Phe	Gln	Asp	Glu					
110				115					120				125							
att	aag	gag	atc	tta	ggt	gtt	ata	tac	aat	gag	cac	aaa	tgc	ttt	cac	433				
Ile	Lys	Glu	Ile	Leu	Gly	Val	Ile	Tyr	Asn	Glu	His	Lys	Cys	Phe	His					
				130					135				140							
aat	aat	gaa	gta	gag	aaa	atg	gat	ttg	tat	ttc	aca	gct	ctt	gga	ttc	481				
Asn	Asn	Glu	Val	Glu	Lys	Met	Asp	Leu	Tyr	Phe	Thr	Ala	Leu	Gly	Phe					
145				150					155											
aga	ctc	ctc	aga	caa	cat	ggt	ttt	aat	att	tcc	caa	gat	gta	ttt	aat	529				
Arg	Leu	Leu	Arg	Gln	His	Gly	Phe	Asn	Ile	Ser	Gln	Asp	Val	Phe	Asn					
160				165					170											
tgt	ttc	aag	aac	gag	aag	ggt	att	gat	ttc	aag	gca	agc	ctt	gct	caa	577				
Cys	Phe	Lys	Asn	Glu	Lys	Gly	Ile	Asp	Phe	Lys	Ala	Ser	Leu	Ala	Gln					
175				180					185											
gat	acg	aag	gga	atg	tta	caa	ctg	tat	gaa	gcg	tct	ttc	ctt	ttg	aga	625				
Asp	Thr	Lys	Gly	Met	Leu	Gln	Leu	Tyr	Glu	Ala	Ser	Phe	Leu	Leu	Arg					
190				195					200				205							
aaa	ggt	gaa	gat	aca	ttg	gag	ctt	gca	aga	gaa	ttt	gcc	aca	aaa	tgt	673				
Lys	Gly	Glu	Asp	Thr	Leu	Glu	Leu	Ala	Arg	Glu	Phe	Ala	Thr	Lys	Cys					
				210					215				220							
ctg	cag	aaa	aaa	ctt	gat	gaa	ggt	ggt	aat	gaa	att	gat	gag	aat	cta	721				
Leu	Gln	Lys	Lys	Leu	Asp	Glu	Gly	Gly	Asn	Glu	Ile	Asp	Glu	Asn	Leu					
225				230					235											
tta	ttg	tgg	att	cgc	cac	tct	ttg	gat	ctt	cct	ctc	cac	tgg	agg	att	769				
Leu	Leu	Trp	Ile	Arg	His	Ser	Leu	Asp	Leu	Pro	Leu	His	Trp	Arg	Ile					

240	245	250	
caa agt gta gag gca aga tgg ttc ata gat gct tat gcg aga agg cca Gln Ser Val Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro 255 260 265			817
gac atg aat cca ctt att ttc gag ctt gcc aaa ctc aac ttc aat att Asp Met Asn Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile 270 275 280 285			865
att caa gca aca cat caa caa gaa ctg aaa gat ctc tcg agg tgg tgg Ile Gln Ala Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp 290 295 300			913
agt aga tta tgc ttc cct gaa aag ctc cca ttt gtg agg gat agg ctc Ser Arg Leu Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu 305 310 315			961
gtt gaa tcc ttc ttt tgg gcg gtt ggg atg ttt gag cca cat caa cat Val Glu Ser Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His 320 325 330			1009
gga tat cag aga aaa atg gcc gcc acc att att gtt tta gca aca gtt Gly Tyr Gln Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val 335 340 345			1057
ata gat gat att tac gat gtg tat ggt acc cta gat gaa cta gaa cta Ile Asp Asp Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu 350 355 360 365			1105
ttt acc gac acg ttt aag aga tgg gat act gaa tca ata acc cga ctt Phe Thr Asp Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu 370 375 380			1153
cct tat tac atg caa tta tgt tat tgg ggt gtc cac aac tat att tcc Pro Tyr Tyr Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser 385 390 395			1201
gat gca gca tat gat att ctc aaa gaa cat ggt ttc ttt tgt ctc caa Asp Ala Ala Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln 400 405 410			1249
tat ctc cgg aaa tcg gtg gta gat ttg gtt gaa gca tat ttt cac gag Tyr Leu Arg Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu 415 420 425			1297
gca aag tgg tac cac agc ggt tat acc cca agc ctg gat gaa tat ctc Ala Lys Trp Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu 430 435 440 445			1345
aac atc gcc aag att tca gtg gcg tct cct gca ata ata tcc cca acc Asn Ile Ala Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr 450 455 460			1393
tat ttc acc ttc gca aac gcg tct cat gac acc gca gtc atc gac agc Tyr Phe Thr Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser 465 470 475			1441
ttg tac caa tat cat gac ata ctt tgc cta gca gga att att ttg agg Leu Tyr Gln Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg			1489

480	485	490	
ctt ccc gac gat ctt ggg aca tca tat ttt gag ctg gcg aga ggc gac Leu Pro Asp Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp 495 500 505			1537
gtg ccg aaa aca atc cag tgc tac atg aag gaa aca aat gct agt gag Val Pro Lys Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu 510 515 520 525			1585
gag gag gcg gtg gag cac gtg aag ttt ctg ata agg gag gcg tgg aag Glu Glu Ala Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys 530 535 540			1633
gat atg aac acg gcc ata gca gcc ggt tat ccg ttt ccg gat ggt atg Asp Met Asn Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met 545 550 555			1681
gtg gcg ggc gca gct aat att ggg cgc gtg gcg cag ttt att tat ctc Val Ala Gly Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu 560 565 570			1729
cac gga gat ggg ttt ggc gtg caa cac tcg aaa acg tac gag cat atc His Gly Asp Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile 575 580 585			1777
gcc ggc cta ctg ttc gag cct tat gca tgaacaaatg ggagactgct Ala Gly Leu Leu Phe Glu Pro Tyr Ala 590 595			1824
tgatatatat taatttggca caccaataat tgcattgttat atatgttgga aaataagtgt			1884
ctggttgaga tgtcatgtgg tgtattatct aaataattca aggttgccctt gtttatgtag			1944
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agctcgagga aaaaaaaaaa			2024
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Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu Leu Val Pro 20 25 30			
Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser Ser Lys Leu 35 40 45			
Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln Pro Ala Leu 50 55 60			
Trp Asp Ser Asn Tyr Ile Gln Ser Ile Asn Thr Pro Tyr Thr Glu Glu 65 70 75 80			

Arg His Leu Asp Arg Lys Ala Glu Leu Ile Val Gln Val Arg Ile Leu
 85 90 95
 Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu Ile His Asp
 100 105 110
 Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu Ile Lys Glu
 115 120 125
 Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His Asn Asn Glu
 130 135 140
 Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Leu Leu
 145 150 155 160
 Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn Cys Phe Lys
 165 170 175
 Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln Asp Thr Lys
 180 185 190
 Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Lys Gly Glu
 195 200 205
 Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys Leu Gln Lys
 210 215 220
 Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu Leu Leu Trp
 225 230 235 240
 Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile Gln Ser Val
 245 250 255
 Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn
 260 265 270
 Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile Ile Gln Ala
 275 280 285
 Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu
 290 295 300
 Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser
 305 310 315 320
 Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln
 325 330 335
 Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp
 340 345 350
 Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu Phe Thr Asp
 355 360 365
 Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu Pro Tyr Tyr
 370 375 380
 Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser Asp Ala Ala
 385 390 395 400

Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln Tyr Leu Arg
 405 410 415
 Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu Ala Lys Trp
 420 425 430
 Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu Asn Ile Ala
 435 440 445
 Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr Tyr Phe Thr
 450 455 460
 Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser Leu Tyr Gln
 465 470 475 480
 Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg Leu Pro Asp
 485 490 495
 Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp Val Pro Lys
 500 505 510
 Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu Glu Glu Ala
 515 520 525
 Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Asp Met Asn
 530 535 540
 Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly
 545 550 555 560
 Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu His Gly Asp
 565 570 575
 Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile Ala Gly Leu
 580 585 590
 Leu Phe Glu Pro Tyr Ala
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<210> 22
 <211> 2024
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 computer-generated nucleic acid sequence

<220>
 <221> CDS
 <222> (11)..(1804)
 <223> computer-generated nucleic acid sequence encoding
 (+)-bornyl diphosphate synthase

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 Met Ser Ile Ile Ser Met Asn Val Ser Ile Leu Ser Lys
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ctt gtc cct tgc act gca ccc acc gct cgc ctc cgg gca tct tgc tcc Leu Val Pro Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser 30 35 40 45	145
tca aaa cta caa gaa gct cat caa atc cga cga tct gga aac tac caa Ser Lys Leu Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln 50 55 60	193
cct gcc ctt tgg gat tcc aat tac att cag tct ctc aat act cca tat Pro Ala Leu Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr 65 70 75	241
acg gag gag agg cac gtg gat aga aaa gca gag ctg att gtg caa gtg Thr Glu Glu Arg His Val Asp Arg Lys Ala Glu Leu Ile Val Gln Val 80 85 90	289
agg ata ctg cta aag gaa aaa atg gag cct gtt caa caa ttg gag ttg Arg Ile Leu Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu 95 100 105	337
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att aag gag atc tta ggt gtt ata tac aat gag cac aaa tgc ttt cac Ile Lys Glu Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His 130 135 140	433
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aga ctc ctc aga caa cat ggt ttt aat att tcc caa gat gta ttt aat Arg Leu Leu Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn 160 165 170	529
tgt ttc aag aac gag aag ggt att gat ttc aag gca agc ctt gct caa Cys Phe Lys Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln 175 180 185	577
gat acg aag gga atg tta caa ctg tat gaa gcg tct ttc ctt ttg aga Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg 190 195 200 205	625
aaa ggt gaa gat aca ttg gag ctt gca aga gaa ttt gcc aca aaa tgt Lys Gly Glu Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys 210 215 220	673
ctg cag aaa aaa ctt gat gaa ggt ggt aat gaa att gat gag aat cta Leu Gln Lys Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu 225 230 235	721
tta ttg tgg att cgc cac tct ttg gat ctt cct ctc cac tgg agg att Leu Leu Trp Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile 240 245 250	769

caa agt gta gag gca aga tgg ttc ata gat gct tat gcg aga agg cca Gln Ser Val Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro 255 260 265	817
gac atg aat cca ctt att ttc gag ctt gcc aaa ctc aac ttc aat att Asp Met Asn Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile 270 275 280 285	865
att caa gca aca cat caa caa gaa ctg aaa gat ctc tcg agg tgg tgg Ile Gln Ala Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp 290 295 300	913
agt aga tta tgc ttc cct gaa aag ctc cca ttt gtg agg gat agg ctc Ser Arg Leu Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu 305 310 315	961
gtt gaa tcc ttc ttt tgg gcg gtt ggg atg ttt gag cca cat caa cat Val Glu Ser Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His 320 325 330	1009
gga tat cag aga aaa atg gcc gcc aca att att gtt tta gca aca gtt Gly Tyr Gln Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val 335 340 345	1057
ata gat gat att tac gat gtg tat ggt aca cta gat gaa cta gaa cta Ile Asp Asp Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu 350 355 360 365	1105
ttt aca gac acg ttt aag aga tgg gat act gaa tca ata acc cga ctt Phe Thr Asp Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu 370 375 380	1153
cct tat tac atg caa tta tgt tat tgg ggt gtc cac aac tat att tcc Pro Tyr Tyr Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser 385 390 395	1201
gat gca gca tat gat att ctc aaa gaa cat ggt ttc ttt tgt ctc caa Asp Ala Ala Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln 400 405 410	1249
tat ctc cgg aaa tcg gtg gta gat ttg gtt gaa gca tat ttt cac gag Tyr Leu Arg Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu 415 420 425	1297
gca aag tgg tac cac agc ggt tat aca cca agc ctg gat gaa tat ctc Ala Lys Trp Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu 430 435 440 445	1345
aac atc gcc aag att tca gtg gcg tct cct gca ata ata tcc cca acc Asn Ile Ala Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr 450 455 460	1393
tat ttc aca ttc gca aac gcg tct cat gac aca gca gtc atc gac agc Tyr Phe Thr Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser 465 470 475	1441
ttg tac caa tat cat gac ata ctt tgc cta gca gga att att ttg agg Leu Tyr Gln Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg 480 485 490	1489

ctt ccc gac gat ctt ggg aca tca tat ttt gag ctg gcg aga ggc gac 1537
 Leu Pro Asp Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp
 495 500 505

gtg ccg aaa aca atc cag tgc tac atg aag gaa aca aat gct agt gag 1585
 Val Pro Lys Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu
 510 515 520 525

gag gag gcg gtg gag cac gtg aag ttt ctg ata agg gag gcg tgg aag 1633
 Glu Glu Ala Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys
 530 535 540

gat atg aac acg gcc ata gca gcc ggt tat ccg ttt ccg gat ggt atg 1681
 Asp Met Asn Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met
 545 550 555

gtg gcg ggc gca gct aat att ggg cgc gtg gcg cag ttt att tat ctc 1729
 Val Ala Gly Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu
 560 565 570

cac gga gat ggg ttt ggc gtg caa cac tcg aaa acg tac gag cat atc 1777
 His Gly Asp Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile
 575 580 585

gcc ggc cta ctg ttc gag cct tat gca tgaacaaatg ggagactgct 1824
 Ala Gly Leu Leu Phe Glu Pro Tyr Ala
 590 595

tgatatatat taatttgga caccaataat tgcattgttat atatgttgga aaataagtgt 1884
 ctgggttgaga tgtcatgtgg tgtattatct aaataattca aggttgccctt gtttatgtag 1944
 ccggtggtgc aactacctcc cattcaaadc aattaaatct aaacagtcga gtcaagctcg 2004
 agctcgagga aaaaaaaaaa 2024

<210> 23
 <211> 598
 <212> PRT
 <213> Artificial Sequence

<400> 23
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 Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu Leu Val Pro
 20 25 30
 Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser Ser Lys Leu
 35 40 45
 Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln Pro Ala Leu
 50 55 60
 Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Thr Glu Glu
 65 70 75 80
 Arg His Val Asp Arg Lys Ala Glu Leu Ile Val Gln Val Arg Ile Leu
 85 90 95

Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu Ile His Asp
 100 105 110
 Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu Ile Lys Glu
 115 120 125
 Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His Asn Asn Glu
 130 135 140
 Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Leu Leu
 145 150 155 160
 Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn Cys Phe Lys
 165 170 175
 Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln Asp Thr Lys
 180 185 190
 Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Lys Gly Glu
 195 200 205
 Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys Leu Gln Lys
 210 215 220
 Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu Leu Leu Trp
 225 230 235 240
 Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile Gln Ser Val
 245 250 255
 Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn
 260 265 270
 Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile Ile Gln Ala
 275 280 285
 Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu
 290 295 300
 Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser
 305 310 315 320
 Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln
 325 330 335
 Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp
 340 345 350
 Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu Phe Thr Asp
 355 360 365
 Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu Pro Tyr Tyr
 370 375 380
 Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser Asp Ala Ala
 385 390 395 400
 Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln Tyr Leu Arg
 405 410 415

Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu Ala Lys Trp
 420 425 430
 Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu Asn Ile Ala
 435 440 445
 Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr Tyr Phe Thr
 450 455 460
 Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser Leu Tyr Gln
 465 470 475 480
 Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg Leu Pro Asp
 485 490 495
 Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp Val Pro Lys
 500 505 510
 Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu Glu Glu Ala
 515 520 525
 Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Asp Met Asn
 530 535 540
 Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly
 545 550 555 560
 Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu His Gly Asp
 565 570 575
 Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile Ala Gly Leu
 580 585 590
 Leu Phe Glu Pro Tyr Ala
 595

<210> 24
 <211> 2024
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 computer-generated nucleic acid sequence

<220>
 <221> CDS
 <222> (11)..(1804)
 <223> computer-generated sequence encoding (+)-bornyl
 diphosphate synthase

<400> 24
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 Met Ser Ile Ile Ser Met Asn Val Ser Ile Leu Ser Lys
 1 5 10
 cca cta aat tgc ctc cac aac ttg gag agg aga cct tca aaa gcc ttg 97
 Pro Leu Asn Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu

15	20	25	
ctt gtc cct tgc act gca ccc acc gct cgc ctc cgg gca tct tgc tcc Leu Val Pro Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser 30 35 40 45			145
tca aaa cta caa gaa gct cat caa atc cga cga tct gga aac tac caa Ser Lys Leu Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln 50 55 60			193
cct gcc ctt tgg gat tcc aat tac att cag tct ctc aat act cca tat Pro Ala Leu Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr 65 70 75			241
acg gag gag agg cac ttg gat aga aaa gca gag gtg att gtg caa gtg Thr Glu Glu Arg His Leu Asp Arg Lys Ala Glu Val Ile Val Gln Val 80 85 90			289
agg ata ctg cta aag gaa aaa atg gag cct gtt caa caa ttg gag ttg Arg Ile Leu Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu 95 100 105			337
att cat gac ttg aaa tat ttg ggg ctc tcg gat ttt ttt caa gat gag Ile His Asp Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu 110 115 120 125			385
att aag gag atc tta ggt gtt ata tac aat gag cac aaa tgc ttt cac Ile Lys Glu Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His 130 135 140			433
aat aat gaa gta gag aaa atg gat ttg tat ttc aca gct ctt gga ttc Asn Asn Glu Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe 145 150 155			481
aga ctc ctc aga caa cat ggt ttt aat att tcc caa gat gta ttt aat Arg Leu Leu Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn 160 165 170			529
tgt ttc aag aac gag aag ggt att gat ttc aag gca agc ctt gct caa Cys Phe Lys Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln 175 180 185			577
gat acg aag gga atg tta caa ctg tat gaa gcg tct ttc ctt ttg aga Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg 190 195 200 205			625
aaa ggt gaa gat aca ttg gag ctt gca aga gaa ttt gcc aca aaa tgt Lys Gly Glu Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys 210 215 220			673
ctg cag aaa aaa ctt gat gaa ggt ggt aat gaa att gat gag aat cta Leu Gln Lys Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu 225 230 235			721
tta ttg tgg att cgc cac tct ttg gat ctt cct ctc cac tgg agg att Leu Leu Trp Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile 240 245 250			769
caa agt gta gag gca aga tgg ttc ata gat gct tat gcg aga agg cca Gln Ser Val Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro 255 260 265 270 275 280 285 290 295 300			817

255	260	265	
gac atg aat cca ctt att ttc gag ctt gcc aaa ctc aac ttc aat att Asp Met Asn Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile 270 275 280 285			865
att caa gca aca cat caa caa gaa ctg aaa gat ctc tcg agg tgg tgg Ile Gln Ala Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp 290 295 300			913
agt aga tta tgc ttc cct gaa aag ctc cca ttt gtg agg gat agg ctc Ser Arg Leu Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu 305 310 315			961
ggt gaa tcc ttc ttt tgg gcg gtt ggg atg ttt gag cca cat caa cat Val Glu Ser Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His 320 325 330			1009
gga tat cag aga aaa atg gcc gcc aca att att gtt tta gca aca gtt Gly Tyr Gln Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val 335 340 345			1057
ata gat gat att tac gat gtg tat ggt aca cta gat gaa cta gaa cta Ile Asp Asp Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu 350 355 360 365			1105
ttt aca gac acg ttt aag aga tgg gat act gaa tca ata acc cga ctt Phe Thr Asp Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu 370 375 380			1153
cct tat tac atg caa tta tgt tat tgg ggt gtc cac aac tat att tcc Pro Tyr Tyr Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser 385 390 395			1201
gat gca gca tat gat att ctc aaa gaa cat ggt ttc ttt tgt ctc caa Asp Ala Ala Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln 400 405 410			1249
tat ctc cgg aaa tcg gtg gta gat ttg gtt gaa gca tat ttt cac gag Tyr Leu Arg Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu 415 420 425			1297
gca aag tgg tac cac agc ggt tat aca cca agc ctg gat gaa tat ctc Ala Lys Trp Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu 430 435 440 445			1345
aac atc gcc aag att tca gtg gcg tct cct gca ata ata tcc cca acc Asn Ile Ala Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr 450 455 460			1393
tat ttc aca ttc gca aac gcg tct cat gac aca gca gtc atc gac agc Tyr Phe Thr Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser 465 470 475			1441
ttg tac caa tat cat gac ata ctt tgc cta gca gga att att ttg agg Leu Tyr Gln Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg 480 485 490			1489
ctt ccc gac gat ctt ggg aca tca tat ttt gag ctg gcg aga ggc gac Leu Pro Asp Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp 1537			

495	500	505	
gtg ccg aaa aca atc	cag tgc tac atg aag gaa aca aat gct agt gag		1585
Val Pro Lys Thr Ile	Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu		
510	515 520	525	
gag gag gcg gtg gag	cac gtg aag ttt ctg ata agg gag gcg tgg aag		1633
Glu Glu Ala Val	Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys		
	530 535	540	
gat atg aac acg gcc ata	gca gcc ggt tat ccg ttt ccg gat ggt atg		1681
Asp Met Asn Thr Ala Ile	Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met		
	545 550	555	
gtg gcg ggc gca gct aat att	ggg cgc gtg gcg cag ttt att tat ctc		1729
Val Ala Gly Ala Ala Asn Ile	Gly Arg Val Ala Gln Phe Ile Tyr Leu		
	560 565	570	
cac gga gat ggg ttt ggc gtg	caa cac tcg aaa acg tac gag cat atc		1777
His Gly Asp Gly Phe Gly Val	Gln His Ser Lys Thr Tyr Glu His Ile		
	575 580	585	
gcc ggc cta ctg ttc gag cct tat	gca tgaacaaatg ggagactgct		1824
Ala Gly Leu Leu Phe Glu Pro Tyr Ala			
	590 595		
tgatatatat taatttggca caccaataat	tgcatgttat atatgttgga aaataagtgt		1884
ctgggttgaga tgtcatgtgg tgtattatct	aaataattca aggttgccctt gtttatgtag		1944
ccggtggtgc aactacctcc cattcaaatc	aattaaatct aaacagtcga gtcaagctcg		2004
agctcgagga aaaaaaaaaa			2024
<210> 25			
<211> 598			
<212> PRT			
<213> Artificial Sequence			
<400> 25			
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Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu Leu Val Pro			
20 25 30			
Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser Ser Lys Leu			
35 40 45			
Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln Pro Ala Leu			
50 55 60			
Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Thr Glu Glu			
65 70 75 80			
Arg His Leu Asp Arg Lys Ala Glu Val Ile Val Gln Val Arg Ile Leu			
85 90 95			
Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu Ile His Asp			

100	105	110
Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu Ile Lys Glu 115 120 125		
Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His Asn Asn Glu 130 135 140		
Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Leu Leu 145 150 155 160		
Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn Cys Phe Lys 165 170 175		
Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln Asp Thr Lys 180 185 190		
Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Lys Gly Glu 195 200 205		
Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys Leu Gln Lys 210 215 220		
Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu Leu Leu Trp 225 230 235 240		
Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile Gln Ser Val 245 250 255		
Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn 260 265 270		
Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile Ile Gln Ala 275 280 285		
Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu 290 295 300		
Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser 305 310 315 320		
Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln 325 330 335		
Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp 340 345 350		
Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu Phe Thr Asp 355 360 365		
Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu Pro Tyr Tyr 370 375 380		
Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser Asp Ala Ala 385 390 395 400		
Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln Tyr Leu Arg 405 410 415		
Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu Ala Lys Trp		

420	425	430
Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu Asn Ile Ala 435 440 445		
Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr Tyr Phe Thr 450 455 460		
Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser Leu Tyr Gln 465 470 475 480		
Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg Leu Pro Asp 485 490 495		
Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp Val Pro Lys 500 505 510		
Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu Glu Glu Ala 515 520 525		
Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Asp Met Asn 530 535 540		
Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly 545 550 555 560		
Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu His Gly Asp 565 570 575		
Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile Ala Gly Leu 580 585 590		
Leu Phe Glu Pro Tyr Ala 595		

<210> 26
 <211> 2024
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 computer-generated nucleic acid sequence

<220>
 <221> CDS
 <222> (11)..(1804)
 <223> computer-generated nucleic acid sequence encoding
 (+)-bornyl diphosphate synthase

<400> 26	
gatcacaaaa atg tct atc att agc atg aac gta tcg atc ctt agc aag	49
Met Ser Ile Ile Ser Met Asn Val Ser Ile Leu Ser Lys	
1 5 10	
cca cta aat tgc ctc cac aac ttg gag agg aga cct tca aaa gcc ttg	97
Pro Leu Asn Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu	
15 20 25	

ctt gtc cct tgc act gca ccc acc gct cgc ctc cgg gca tct tgc tcc Leu Val Pro Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser 30 35 40 45	145
tca aaa cta caa gaa gct cat caa atc cga cga tct gga aac tac caa Ser Lys Leu Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln 50 55 60	193
cct gcc ctt tgg gat tcc aat tac att cag tct ctc aat act cca tat Pro Ala Leu Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr 65 70 75	241
acg gag gag agg cac ttg gat aga aaa gca gag ctg att ctg caa gtg Thr Glu Glu Arg His Leu Asp Arg Lys Ala Glu Leu Ile Leu Gln Val 80 85 90	289
agg ata ctg cta aag gaa aaa atg gag cct gtt caa caa ttg gag ttg Arg Ile Leu Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu 95 100 105	337
att cat gac ttg aaa tat ttg ggg ctc tcg gat ttt ttt caa gat gag Ile His Asp Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu 110 115 120 125	385
att aag gag atc tta ggt gtt ata tac aat gag cac aaa tgc ttt cac Ile Lys Glu Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His 130 135 140	433
aat aat gaa gta gag aaa atg gat ttg tat ttc aca gct ctt gga ttc Asn Asn Glu Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe 145 150 155	481
aga ctc ctc aga caa cat ggt ttt aat att tcc caa gat gta ttt aat Arg Leu Leu Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn 160 165 170	529
tgt ttc aag aac gag aag ggt att gat ttc aag gca agc ctt gct caa Cys Phe Lys Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln 175 180 185	577
gat acg aag gga atg tta caa ctg tat gaa gcg tct ttc ctt ttg aga Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg 190 195 200 205	625
aaa ggt gaa gat aca ttg gag ctt gca aga gaa ttt gcc aca aaa tgt Lys Gly Glu Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys 210 215 220	673
ctg cag aaa aaa ctt gat gaa ggt ggt aat gaa att gat gag aat cta Leu Gln Lys Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu 225 230 235	721
tta ttg tgg att cgc cac tct ttg gat ctt cct ctc cac tgg agg att Leu Leu Trp Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile 240 245 250	769
caa agt gta gag gca aga tgg ttc ata gat gct tat gcg aga agg cca Gln Ser Val Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro 255 260 265	817

gac atg aat cca ctt att ttc gag ctt gcc aaa ctc aac ttc aat att Asp Met Asn Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile 270 275 280 285	865
att caa gca aca cat caa caa gaa ctg aaa gat ctc tcg agg tgg tgg Ile Gln Ala Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp 290 295 300	913
agt aga tta tgc ttc cct gaa aag ctc cca ttt gtg agg gat agg ctc Ser Arg Leu Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu 305 310 315	961
gtt gaa tcc ttc ttt tgg gcg gtt ggg atg ttt gag cca cat caa cat Val Glu Ser Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His 320 325 330	1009
gga tat cag aga aaa atg gcc gcc aca att att gtt tta gca aca gtt Gly Tyr Gln Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val 335 340 345	1057
ata gat gat att tac gat gtg tat ggt aca cta gat gaa cta gaa cta Ile Asp Asp Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu 350 355 360 365	1105
ttt aca gac acg ttt aag aga tgg gat act gaa tca ata acc cga ctt Phe Thr Asp Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu 370 375 380	1153
cct tat tac atg caa tta tgt tat tgg ggt gtc cac aac tat att tcc Pro Tyr Tyr Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser 385 390 395	1201
gat gca gca tat gat att ctc aaa gaa cat ggt ttc ttt tgt ctc caa Asp Ala Ala Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln 400 405 410	1249
tat ctc cgg aaa tcg gtg gta gat ttg gtt gaa gca tat ttt cac gag Tyr Leu Arg Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu 415 420 425	1297
gca aag tgg tac cac agc ggt tat aca cca agc ctg gat gaa tat ctc Ala Lys Trp Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu 430 435 440 445	1345
aac atc gcc aag att tca gtg gcg tct cct gca ata ata tcc cca acc Asn Ile Ala Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr 450 455 460	1393
tat ttc aca ttc gca aac gcg tct cat gac aca gca gtc atc gac agc Tyr Phe Thr Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser 465 470 475	1441
ttg tac caa tat cat gac ata ctt tgc cta gca gga att att ttg agg Leu Tyr Gln Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg 480 485 490	1489
ctt ccc gac gat ctt ggg aca tca tat ttt gag ctg gcg aga ggc gac Leu Pro Asp Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp 495 500 505	1537

gtg ccg aaa aca atc cag tgc tac atg aag gaa aca aat gct agt gag 1585
 Val Pro Lys Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu
 510 515 520 525
 gag gag gcg gtg gag cac gtg aag ttt ctg ata agg gag gcg tgg aag 1633
 Glu Glu Ala Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys
 530 535 540
 gat atg aac acg gcc ata gca gcc ggt tat ccg ttt ccg gat ggt atg 1681
 Asp Met Asn Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met
 545 550 555
 gtg gcg ggc gca gct aat att ggg cgc gtg gcg cag ttt att tat ctc 1729
 Val Ala Gly Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu
 560 565 570
 cac gga gat ggg ttt ggc gtg caa cac tcg aaa acg tac gag cat atc 1777
 His Gly Asp Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile
 575 580 585
 gcc ggc cta ctg ttc gag cct tat gca tgaacaaatg ggagactgct 1824
 Ala Gly Leu Leu Phe Glu Pro Tyr Ala
 590 595
 tgatatatat taatttggca caccaataat tgcattgttat atatgttgga aaataagtgt 1884
 ctgggttgaga tgtcatgtgg tgtattatct aaataattca aggttgcctt gtttatgtag 1944
 ccggtggtgc aactacctcc cattcaaatac aattaaatct aaacagtcga gtcaagctcg 2004
 agctcgagga aaaaaaaaaa 2024

<210> 27

<211> 598

<212> PRT

<213> Artificial Sequence

<400> 27

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 Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu Leu Val Pro
 20 25 30
 Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser Ser Lys Leu
 35 40 45
 Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln Pro Ala Leu
 50 55 60
 Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Thr Glu Glu
 65 70 75 80
 Arg His Leu Asp Arg Lys Ala Glu Leu Ile Leu Gln Val Arg Ile Leu
 85 90 95
 Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu Ile His Asp
 100 105 110

Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu Ile Lys Glu
 115 120 125
 Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His Asn Asn Glu
 130 135 140
 Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Leu Leu
 145 150 155 160
 Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn Cys Phe Lys
 165 170 175
 Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln Asp Thr Lys
 180 185 190
 Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Lys Gly Glu
 195 200 205
 Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys Leu Gln Lys
 210 215 220
 Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu Leu Leu Trp
 225 230 235 240
 Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile Gln Ser Val
 245 250 255
 Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn
 260 265 270
 Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile Ile Gln Ala
 275 280 285
 Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu
 290 295 300
 Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser
 305 310 315 320
 Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln
 325 330 335
 Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp
 340 345 350
 Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu Phe Thr Asp
 355 360 365
 Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu Pro Tyr Tyr
 370 375 380
 Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser Asp Ala Ala
 385 390 395 400
 Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln Tyr Leu Arg
 405 410 415
 Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu Ala Lys Trp
 420 425 430

Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu Asn Ile Ala
 435 440 445
 Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr Tyr Phe Thr
 450 455 460
 Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser Leu Tyr Gln
 465 470 475 480
 Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg Leu Pro Asp
 485 490 495
 Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp Val Pro Lys
 500 505 510
 Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu Glu Glu Ala
 515 520 525
 Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Asp Met Asn
 530 535 540
 Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly
 545 550 555 560
 Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu His Gly Asp
 565 570 575
 Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile Ala Gly Leu
 580 585 590
 Leu Phe Glu Pro Tyr Ala
 595

<210> 28

<211> 2024

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 computer-generated nucleic acid sequence

<220>

<221> CDS

<222> (11)..(1804)

<223> computer-generated nucleic acid sequence encoding
 (+)-bornyl diphosphate synthase

<400> 28

gatcacaaaa atg tct atc att agc atg aac gta tcg atc ctt agc aag 49
 Met Ser Ile Ile Ser Met Asn Val Ser Ile Leu Ser Lys
 1 5 10

cca cta aat tgc ctc cac aac ttg gag agg aga cct tca aaa gcc ttg 97
 Pro Leu Asn Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu
 15 20 25

ctt gtc cct tgc act gca ccc acc gct cgc ctc cgg gca tct tgc tcc 145
 Leu Val Pro Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser

30	35	40	45	
tca aaa cta caa gaa gct cat caa atc cga cga tct gga aac tac caa Ser Lys Leu Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln	50	55	60	193
cct gcc ctt tgg gat tcc aat tac att cag tct ctc aat act cca tat Pro Ala Leu Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr	65	70	75	241
acg gag gag agg cac ttg gat aga aaa gca gag ctg att gtg caa gtg Thr Glu Glu Arg His Leu Asp Arg Lys Ala Glu Leu Ile Val Gln Val	80	85	90	289
agg cta ctg cta aag gaa aaa atg gag cct gtt caa caa ttg gag ttg Arg Leu Leu Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu	95	100	105	337
att cat gac ttg aaa tat ttg ggg ctc tcg gat ttt ttt caa gat gag Ile His Asp Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu	110	115	120	385
att aag gag atc tta ggt gtt ata tac aat gag cac aaa tgc ttt cac Ile Lys Glu Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His	130	135	140	433
aat aat gaa gta gag aaa atg gat ttg tat ttc aca gct ctt gga ttc Asn Asn Glu Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe	145	150	155	481
aga ctc ctc aga caa cat ggt ttt aat att tcc caa gat gta ttt aat Arg Leu Leu Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn	160	165	170	529
tgt ttc aag aac gag aag ggt att gat ttc aag gca agc ctt gct caa Cys Phe Lys Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln	175	180	185	577
gat acg aag gga atg tta caa ctg tat gaa gcg tct ttc ctt ttg aga Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg	190	195	200	625
aaa ggt gaa gat aca ttg gag ctt gca aga gaa ttt gcc aca aaa tgt Lys Gly Glu Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys	210	215	220	673
ctg cag aaa aaa ctt gat gaa ggt ggt aat gaa att gat gag aat cta Leu Gln Lys Lys Leu Asp Glu Gly Gln Asn Glu Ile Asp Glu Asn Leu	225	230	235	721
tta ttg tgg att cgc cac tct ttg gat ctt cct ctc cac tgg agg att Leu Leu Trp Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile	240	245	250	769
caa agt gta gag gca aga tgg ttc ata gat gct tat gcg aga agg cca Gln Ser Val Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro	255	260	265	817
gac atg aat cca ctt att ttc gag ctt gcc aaa ctc aac ttc aat att Asp Met Asn Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile				865

270	275	280	285	
att caa gca aca cat Ile Gln Ala Thr	caa caa gaa ctg Gln Gln Glu Leu	aaa gat ctc tcg Lys Asp Leu Ser	agg tgg tgg Arg Trp Trp	913
	290	295	300	
agt aga tta tgc ttc cct Ser Arg Leu Cys	gaa aag ctc cca Glu Lys Leu Pro	ttt gtg agg gat Phe Val Arg Asp	agg ctc Arg Leu	961
	305	310	315	
gtt gaa tcc ttc ttt tgg Val Glu Ser Phe	gcg gtt ggg atg Ala Val Gly Met	ttt gag cca cat Phe Glu Pro His	caa cat Gln His	1009
	320	325	330	
gga tat cag aga aaa atg Gly Tyr Gln Arg	gcc gcc aca att Ala Ala Thr Ile	att gtt tta gca Ile Val Leu Ala	aca gtt Thr Val	1057
	335	340	345	
ata gat gat att tac Ile Asp Asp Ile	gat gtg tat ggt Asp Val Tyr Gly	aca cta gat gaa Thr Leu Asp Glu	cta gaa cta Leu Glu Leu	1105
	355	360	365	
ttt aca gac acg ttt Phe Thr Asp Thr	aag aga tgg gat Lys Arg Trp Asp	act gaa tca ata Thr Glu Ser Ile	acc cga ctt Thr Arg Leu	1153
	370	375	380	
cct tat tac atg caa tta Pro Tyr Tyr Met	tgt tat tgg ggt Leu Cys Tyr Trp	gtc cac aac tat Val His Asn Tyr	att tcc Ile Ser	1201
	385	390	395	
gat gca gca tat gat Asp Ala Ala Tyr	att ctc aaa gaa Ile Leu Lys Glu	cat ggt ttc ttt His Gly Phe Phe	tgt ctc caa Cys Leu Gln	1249
	400	405	410	
tat ctc cgg aaa tcg Tyr Leu Arg Lys	gtg gta gat ttg Val Val Asp Leu	gtt gaa gca tat Val Glu Ala Tyr	ttt cac gag Phe His Glu	1297
	415	420	425	
gca aag tgg tac cac Ala Lys Trp Tyr	agc ggt tat aca His Ser Gly Tyr	cca agc ctg gat Pro Ser Leu Asp	gaa tat ctc Glu Tyr Leu	1345
	435	440	445	
aac atc gcc aag att Asn Ile Ala Lys	tca gtg gcg tct Ser Val Ala Ser	cct gca ata ata Pro Ala Ile Ile	tcc cca acc Ser Pro Thr	1393
	450	455	460	
tat ttc aca ttc gca Tyr Phe Thr Phe	aac gcg tct cat Ala Asn Ala Ser	gac aca gca gtc His Asp Thr Ala	atc gac agc Val Ile Asp Ser	1441
	465	470	475	
ttg tac caa tat cat Leu Tyr Gln Tyr	gac ata ctt tgc His Asp Ile Leu	cta gca gga att Leu Ala Gly Ile	att ttg agg Ile Ile Leu Arg	1489
	480	485	490	
ctt ccc gac gat ctt Leu Pro Asp Asp	ggg aca tca tat Leu Gly Thr Ser	ttt gag ctg gcg Phe Glu Leu Ala	aga ggc gac Arg Gly Asp	1537
	495	500	505	
gtg ccg aaa aca atc Val Pro Lys Thr	cag tgc tac atg Gln Cys Tyr Met	aag gaa aca aat Lys Glu Thr Asn	gct agt gag Ala Ser Glu	1585

510 515 520 525
 gag gag gcg gtg gag cac gtg aag ttt ctg ata agg gag gcg tgg aag 1633
 Glu Glu Ala Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys
 530 535 540
 gat atg aac acg gcc ata gca gcc ggt tat ccg ttt ccg gat ggt atg 1681
 Asp Met Asn Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met
 545 550 555
 gtg gcg ggc gca gct aat att ggg cgc gtg gcg cag ttt att tat ctc 1729
 Val Ala Gly Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu
 560 565 570
 cac gga gat ggg ttt ggc gtg caa cac tcg aaa acg tac gag cat atc 1777
 His Gly Asp Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile
 575 580 585
 gcc ggc cta ctg ttc gag cct tat gca tgaacaaatg ggagactgct 1824
 Ala Gly Leu Leu Phe Glu Pro Tyr Ala
 590 595
 tgatatatat taatttggca caccaataat tgcattgttat atatgttgga aaataagtgt 1884
 ctgggtgaga tgcattgttg tgtattatct aaataattca aggttgccctt gtttatgtag 1944
 ccggtggtgc aactacctcc cattcaaattc aattaaattc aaacagtcga gtcaagctcg 2004
 agctcgagga aaaaaaaaaa 2024

 <210> 29
 <211> 598
 <212> PRT
 <213> Artificial Sequence

 <400> 29
 Met Ser Ile Ile Ser Met Asn Val Ser Ile Leu Ser Lys Pro Leu Asn
 1 5 10 15
 Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu Leu Val Pro
 20 25 30
 Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser Ser Lys Leu
 35 40 45
 Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln Pro Ala Leu
 50 55 60
 Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Thr Glu Glu
 65 70 75 80
 Arg His Leu Asp Arg Lys Ala Glu Leu Ile Val Gln Val Arg Leu Leu
 85 90 95
 Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu Ile His Asp
 100 105 110
 Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu Ile Lys Glu
 115 120 125

Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His Asn Asn Glu
 130 135 140
 Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Leu Leu
 145 150 155 160
 Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn Cys Phe Lys
 165 170 175
 Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln Asp Thr Lys
 180 185 190
 Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Lys Gly Glu
 195 200 205
 Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys Leu Gln Lys
 210 215 220
 Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu Leu Leu Trp
 225 230 235 240
 Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile Gln Ser Val
 245 250 255
 Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn
 260 265 270
 Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile Ile Gln Ala
 275 280 285
 Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu
 290 295 300
 Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser
 305 310 315 320
 Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln
 325 330 335
 Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp
 340 345 350
 Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu Phe Thr Asp
 355 360 365
 Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu Pro Tyr Tyr
 370 375 380
 Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser Asp Ala Ala
 385 390 395 400
 Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln Tyr Leu Arg
 405 410 415
 Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu Ala Lys Trp
 420 425 430
 Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu Asn Ile Ala
 435 440 445

Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr Tyr Phe Thr
 450 455 460
 Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser Leu Tyr Gln
 465 470 475 480
 Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg Leu Pro Asp
 485 490 495
 Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp Val Pro Lys
 500 505 510
 Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu Glu Glu Ala
 515 520 525
 Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Asp Met Asn
 530 535 540
 Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly
 545 550 555 560
 Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu His Gly Asp
 565 570 575
 Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile Ala Gly Leu
 580 585 590
 Leu Phe Glu Pro Tyr Ala
 595

<210> 30
 <211> 2024
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 computer-generated nucleic acid sequence

<220>
 <221> CDS
 <222> (11)..(1804)
 <223> computer-generated nucleic acid sequence encoding
 (+)-bornyl diphosphate synthase

<400> 30
 gatcacaaaa atg tct atc att agc atg aac gta tcg atc ctt agc aag 49
 Met Ser Ile Ile Ser Met Asn Val Ser Ile Leu Ser Lys
 1 5 10
 cca cta aat tgc ctc cac aac ttg gag agg aga cct tca aaa gcc ttg 97
 Pro Leu Asn Cys Leu His Asn Ser Leu Glu Arg Arg Pro Ser Lys Ala Leu
 15 20 25
 ctt gtc cct tgc act gca ccc acc gct cgc ctc cgg gca tct tgc tcc 145
 Leu Val Pro Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser
 30 35 40 45

tca aaa cta caa gaa gct cat caa atc cga cga tct gga aac tac caa Ser Lys Leu Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln 50 55 60	193
cct gcc ctt tgg gat tcc aat tac att cag tct ctc aat act cca tat Pro Ala Leu Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr 65 70 75	241
acg gag gag agg cac ttg gat aga aaa gca gag ctg att gtg caa gtg Thr Glu Glu Arg His Leu Asp Arg Lys Ala Glu Leu Ile Val Gln Val 80 85 90	289
agg ata gtg cta aag gaa aaa atg gag cct gtt caa caa ttg gag ttg Arg Ile Val Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu 95 100 105	337
att cat gac ttg aaa tat ttg ggg ctc tcg gat ttt ttt caa gat gag Ile His Asp Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu 110 115 120 125	385
att aag gag atc tta ggt gtt ata tac aat gag cac aaa tgc ttt cac Ile Lys Glu Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His 130 135 140	433
aat aat gaa gta gag aaa atg gat ttg tat ttc aca gct ctt gga ttc Asn Asn Glu Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe 145 150 155	481
aga ctc ctc aga caa cat ggt ttt aat att tcc caa gat gta ttt aat Arg Leu Leu Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn 160 165 170	529
tgt ttc aag aac gag aag ggt att gat ttc aag gca agc ctt gct caa Cys Phe Lys Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln 175 180 185	577
gat acg aag gga atg tta caa ctg tat gaa gcg tct ttc ctt ttg aga Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg 190 195 200 205	625
aaa ggt gaa gat aca ttg gag ctt gca aga gaa ttt gcc aca aaa tgt Lys Gly Glu Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys 210 215 220	673
ctg cag aaa aaa ctt gat gaa ggt ggt aat gaa att gat gag aat cta Leu Gln Lys Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu 225 230 235	721
tta ttg tgg att cgc cac tct ttg gat ctt cct ctc cac tgg agg att Leu Leu Trp Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile 240 245 250	769
caa agt gta gag gca aga tgg ttc ata gat gct tat gcg aga agg cca Gln Ser Val Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro 255 260 265	817
gac atg aat cca ctt att ttc gag ctt gcc aaa ctc aac ttc aat att Asp Met Asn Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile 270 275 280 285	865

att caa gca aca cat caa caa gaa ctg aaa gat ctc tcg agg tgg tgg Ile Gln Ala Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp 290 295 300	913
agt aga tta tgc ttc cct gaa aag ctc cca ttt gtg agg gat agg ctc Ser Arg Leu Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu 305 310 315	961
gtt gaa tcc ttc ttt tgg gcg gtt ggg atg ttt gag cca cat caa cat Val Glu Ser Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His 320 325 330	1009
gga tat cag aga aaa atg gcc gcc aca att att gtt tta gca aca gtt Gly Tyr Gln Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val 335 340 345	1057
ata gat gat att tac gat gtg tat ggt aca cta gat gaa cta gaa cta Ile Asp Asp Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu 350 355 360 365	1105
ttt aca gac acg ttt aag aga tgg gat act gaa tca ata acc cga ctt Phe Thr Asp Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu 370 375 380	1153
cct tat tac atg caa tta tgt tat tgg ggt gtc cac aac tat att tcc Pro Tyr Tyr Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser 385 390 395	1201
gat gca gca tat gat att ctc aaa gaa cat ggt ttc ttt tgt ctc caa Asp Ala Ala Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln 400 405 410	1249
tat ctc cgg aaa tcg gtg gta gat ttg gtt gaa gca tat ttt cac gag Tyr Leu Arg Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu 415 420 425	1297
gca aag tgg tac cac agc ggt tat aca cca agc ctg gat gaa tat ctc Ala Lys Trp Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu 430 435 440 445	1345
aac atc gcc aag att tca gtg gcg tct cct gca ata ata tcc cca acc Asn Ile Ala Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr 450 455 460	1393
tat ttc aca ttc gca aac gcg tct cat gac aca gca gtc atc gac agc Tyr Phe Thr Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser 465 470 475	1441
ttg tac caa tat cat gac ata ctt tgc cta gca gga att att ttg agg Leu Tyr Gln Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg 480 485 490	1489
ctt ccc gac gat ctt ggg aca tca tat ttt gag ctg gcg aga ggc gac Leu Pro Asp Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp 495 500 505	1537
gtg ccg aaa aca atc cag tgc tac atg aag gaa aca aat gct agt gag Val Pro Lys Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu 510 515 520 525	1585

gag gag gcg gtg gag cac gtg aag ttt ctg ata agg gag gcg tgg aag 1633
 Glu Glu Ala Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys
 530 535 540
 gat atg aac acg gcc ata gca gcc ggt tat ccg ttt ccg gat ggt atg 1681
 Asp Met Asn Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met
 545 550 555
 gtg gcg ggc gca gct aat att ggg cgc gtg gcg cag ttt att tat ctc 1729
 Val Ala Gly Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu
 560 565 570
 cac gga gat ggg ttt ggc gtg caa cac tcg aaa acg tac gag cat atc 1777
 His Gly Asp Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile
 575 580 585
 gcc ggc cta ctg ttc gag cct tat gca tgaacaaatg ggagactgct 1824
 Ala Gly Leu Leu Phe Glu Pro Tyr Ala
 590 595
 tgatatatat taatttggca caccaataat tgcattgttat atatgttgga aaataagtgt 1884
 ctgggttgaga tgtcatgtgg tgtattatct aaataattca aggttgcctt gtttatgtag 1944
 ccggtggtgc aactacctcc cattcaaadc aattaaatct aaacagtcga gtcaagctcg 2004
 agctcgagga aaaaaaaaaa 2024

<210> 31
 <211> 598
 <212> PRT
 <213> Artificial Sequence

<400> 31
 Met Ser Ile Ile Ser Met Asn Val Ser Ile Leu Ser Lys Pro Leu Asn
 1 5 10 15
 Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu Leu Val Pro
 20 25 30
 Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser Ser Lys Leu
 35 40 45
 Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln Pro Ala Leu
 50 55 60
 Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Thr Glu Glu
 65 70 75 80
 Arg His Leu Asp Arg Lys Ala Glu Leu Ile Val Gln Val Arg Ile Val
 85 90 95
 Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu Ile His Asp
 100 105 110
 Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu Ile Lys Glu
 115 120 125
 Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His Asn Asn Glu

130	135	140
Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Leu Leu 145 150 155 160		
Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn Cys Phe Lys 165 170 175		
Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln Asp Thr Lys 180 185 190		
Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Lys Gly Glu 195 200 205		
Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys Leu Gln Lys 210 215 220		
Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu Leu Leu Trp 225 230 235 240		
Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile Gln Ser Val 245 250 255		
Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn 260 265 270		
Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile Ile Gln Ala 275 280 285		
Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu 290 295 300		
Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser 305 310 315 320		
Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln 325 330 335		
Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp 340 345 350		
Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu Phe Thr Asp 355 360 365		
Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu Pro Tyr Tyr 370 375 380		
Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser Asp Ala Ala 385 390 395 400		
Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln Tyr Leu Arg 405 410 415		
Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu Ala Lys Trp 420 425 430		
Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu Asn Ile Ala 435 440 445		
Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr Tyr Phe Thr		

450 455 460
 Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser Leu Tyr Gln
 465 470 475 480
 Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg Leu Pro Asp
 485 490 495
 Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp Val Pro Lys
 500 505 510
 Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu Glu Glu Ala
 515 520 525
 Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Asp Met Asn
 530 535 540
 Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly
 545 550 555 560
 Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu His Gly Asp
 565 570 575
 Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile Ala Gly Leu
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 Leu Phe Glu Pro Tyr Ala
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<210> 32

<211> 2024

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:
 computer-generated nucleic acid sequence

<220>

<221> CDS

<222> (11)..(1804)

 <223> computer-generated nucleic acid sequence encoding
 (+)-bornyl diphosphate synthase

<400> 32

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 Pro Leu Asn Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu
 15 20 25

 ctt gtc cct tgc act gca ccc acc gct cgc ctc cgg gca tct tgc tcc 145
 Leu Val Pro Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser
 30 35 40 45

 tca aaa cta caa gaa gct cat caa atc cga cga tct gga aac tac caa 193
 Ser Lys Leu Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln

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Arg	Ile	Leu	Ile	Lys	Glu	Lys	Met	Glu	Pro	Val	Gln	Gln	Leu	Glu	Leu															
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Asn	Asn	Glu	Val	Glu	Lys	Met	Asp	Leu	Tyr	Phe	Thr	Ala	Leu	Gly	Phe															
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Arg	Leu	Leu	Arg	Gln	His	Gly	Phe	Asn	Ile	Ser	Gln	Asp	Val	Phe	Asn															
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tgt	ttc	aag	aac	gag	aag	ggg	att	gat	ttc	aag	gca	agc	ctt	gct	caa	577														
Cys	Phe	Lys	Asn	Glu	Lys	Gly	Ile	Asp	Phe	Lys	Ala	Ser	Leu	Ala	Gln															
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gat	acg	aag	gga	atg	tta	caa	ctg	tat	gaa	gcg	tct	ttc	ctt	ttg	aga	625														
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190				195						200					205															
aaa	ggg	gaa	gat	aca	ttg	gag	ctt	gca	aga	gaa	ttt	gcc	aca	aaa	tgt	673														
Lys	Gly	Glu	Asp	Thr	Leu	Glu	Leu	Ala	Arg	Glu	Phe	Ala	Thr	Lys	Cys															
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ctg	cag	aaa	aaa	ctt	gat	gaa	ggg	ggg	aat	gaa	att	gat	gag	aat	cta	721														
Leu	Gln	Lys	Lys	Leu	Asp	Glu	Gly	Gly	Asn	Glu	Ile	Asp	Glu	Asn	Leu															
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290										295										300									
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Ser	Arg	Leu	Cys	Phe	Pro	Glu	Lys	Leu	Pro	Phe	Val	Arg	Asp	Arg	Leu														
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ggt	gaa	tcc	ttc	ttt	tgg	gcg	gtt	ggg	atg	ttt	gag	cca	cat	caa	cat					1009									
Val	Glu	Ser	Phe	Phe	Trp	Ala	Val	Gly	Met	Phe	Glu	Pro	His	Gln	His														
			320				325					330																	
gga	tat	cag	aga	aaa	atg	gcc	gcc	aca	att	att	gtt	tta	gca	aca	gtt					1057									
Gly	Tyr	Gln	Arg	Lys	Met	Ala	Ala	Thr	Ile	Ile	Val	Leu	Ala	Thr	Val														
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ata	gat	gat	att	tac	gat	gtg	tat	ggt	aca	cta	gat	gaa	cta	gaa	cta					1105									
Ile	Asp	Asp	Ile	Tyr	Asp	Val	Tyr	Gly	Thr	Leu	Asp	Glu	Leu	Glu	Leu														
					355					360					365														
ttt	aca	gac	acg	ttt	aag	aga	tgg	gat	act	gaa	tca	ata	acc	cga	ctt					1153									
Phe	Thr	Asp	Thr	Phe	Lys	Arg	Trp	Asp	Thr	Glu	Ser	Ile	Thr	Arg	Leu														
				370					375					380															
cct	tat	tac	atg	caa	tta	tgt	tat	tgg	ggt	gtc	cac	aac	tat	att	tcc					1201									
Pro	Tyr	Tyr	Met	Gln	Leu	Cys	Tyr	Trp	Gly	Val	His	Asn	Tyr	Ile	Ser														
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gat	gca	gca	tat	gat	att	ctc	aaa	gaa	cat	ggt	ttc	ttt	tgt	ctc	caa					1249									
Asp	Ala	Ala	Tyr	Asp	Ile	Leu	Lys	Glu	His	Gly	Phe	Phe	Cys	Leu	Gln														
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tat	ctc	cgg	aaa	tcg	gtg	gta	gat	ttg	gtt	gaa	gca	tat	ttt	cac	gag					1297									
Tyr	Leu	Arg	Lys	Ser	Val	Val	Asp	Leu	Val	Glu	Ala	Tyr	Phe	His	Glu														
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gca	aag	tgg	tac	cac	agc	ggt	tat	aca	cca	agc	ctg	gat	gaa	tat	ctc					1345									
Ala	Lys	Trp	Tyr	His	Ser	Gly	Tyr	Thr	Pro	Ser	Leu	Asp	Glu	Tyr	Leu														
					435					440					445														
aac	atc	gcc	aag	att	tca	gtg	gcg	tct	cct	gca	ata	ata	tcc	cca	acc					1393									
Asn	Ile	Ala	Lys	Ile	Ser	Val	Ala	Ser	Pro	Ala	Ile	Ile	Ser	Pro	Thr														
				450					455					460															
tat	ttc	aca	ttc	gca	aac	gcg	tct	cat	gac	aca	gca	gtc	atc	gac	agc					1441									
Tyr	Phe	Thr	Phe	Ala	Asn	Ala	Ser	His	Asp	Thr	Ala	Val	Ile	Asp	Ser														
			465				470						475																
ttg	tac	caa	tat	cat	gac	ata	ctt	tgc	cta	gca	gga	att	att	ttg	agg					1489									
Leu	Tyr	Gln	Tyr	His	Asp	Ile	Leu	Cys	Leu	Ala	Gly	Ile	Ile	Leu	Arg														
			480				485					490																	
ctt	ccc	gac	gat	ctt	ggg	aca	tca	tat	ttt	gag	ctg	gcg	aga	ggc	gac					1537									
Leu	Pro	Asp	Asp	Leu	Gly	Thr	Ser	Tyr	Phe	Glu	Leu	Ala	Arg	Gly	Asp														
			495			500					505																		
gtg	ccg	aaa	aca	atc	cag	tgc	tac	atg	aag	gaa	aca	aat	gct	agt	gag					1585									
Val	Pro	Lys	Thr	Ile	Gln	Cys	Tyr	Met	Lys	Glu	Thr	Asn	Ala	Ser	Glu														
					515					520				525															
gag	gag	gcg	gtg	gag	cac	gtg	aag	ttt	ctg	ata	agg	gag	gcg	tgg	aag					1633									
Glu	Glu	Ala	Val	Glu	His	Val	Lys	Phe	Leu	Ile	Arg	Glu	Ala	Trp	Lys														

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      530              535              540
gat atg aac acg gcc ata gca gcc ggt tat ccg ttt ccg gat ggt atg 1681
Asp Met Asn Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met
      545              550              555

gtg gcg ggc gca gct aat att ggg cgc gtg gcg cag ttt att tat ctc 1729
Val Ala Gly Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu
      560              565              570

cac gga gat ggg ttt ggc gtg caa cac tcg aaa acg tac gag cat atc 1777
His Gly Asp Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile
      575              580              585

gcc ggc cta ctg ttc gag cct tat gca tgaacaaatg ggagactgct 1824
Ala Gly Leu Leu Phe Glu Pro Tyr Ala
      590              595

tgatatatat taatttggca caccaataat tgcattgttat atatgttgga aaataagtgt 1884

ctggttgaga tgtcatgtgg tgtattatct aaataattca aggttgcctt gtttatgtag 1944

ccggtggtgc aactacctcc cattcaaadc aattaaatct aaacagtcga gtcaagctcg 2004

agctcgagga aaaaaaaaaa 2024

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<211> 598
<212> PRT
<213> Artificial Sequence

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      20          25          30
Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser Ser Lys Leu
      35          40          45
Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln Pro Ala Leu
      50          55          60
Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Thr Glu Glu
      65          70          75          80
Arg His Leu Asp Arg Lys Ala Glu Leu Ile Val Gln Val Arg Ile Leu
      85          90          95
Ile Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu Ile His Asp
      100         105         110
Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu Ile Lys Glu
      115         120         125
Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His Asn Asn Glu
      130         135         140

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Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Leu Leu
 145 150 155 160
 Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn Cys Phe Lys
 165 170 175
 Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln Asp Thr Lys
 180 185 190
 Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Lys Gly Glu
 195 200 205
 Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys Leu Gln Lys
 210 215 220
 Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu Leu Leu Trp
 225 230 235 240
 Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile Gln Ser Val
 245 250 255
 Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn
 260 265 270
 Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile Ile Gln Ala
 275 280 285
 Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu
 290 295 300
 Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser
 305 310 315 320
 Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln
 325 330 335
 Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp
 340 345 350
 Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu Phe Thr Asp
 355 360 365
 Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu Pro Tyr Tyr
 370 375 380
 Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser Asp Ala Ala
 385 390 395 400
 Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln Tyr Leu Arg
 405 410 415
 Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu Ala Lys Trp
 420 425 430
 Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu Asn Ile Ala
 435 440 445
 Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr Tyr Phe Thr
 450 455 460

Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser Leu Tyr Gln
 465 470 475 480
 Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg Leu Pro Asp
 485 490 495
 Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp Val Pro Lys
 500 505 510
 Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu Glu Glu Ala
 515 520 525
 Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Asp Met Asn
 530 535 540
 Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly
 545 550 555 560
 Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu His Gly Asp
 565 570 575
 Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile Ala Gly Leu
 580 585 590
 Leu Phe Glu Pro Tyr Ala
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<210> 34
 <211> 598
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 computer-generated protein sequence

<220>
 <221> VARIANT
 <222> (1)..(598)
 <223> Computer-generated (+)-bornyl diphosphate synthase
 protein variant

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 20 25 30
 Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser Ser Lys Leu
 35 40 45
 Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln Pro Ala Ile
 50 55 60
 Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Thr Glu Glu
 65 70 75 80
 Arg His Leu Asp Arg Lys Ala Glu Leu Ile Val Gln Val Arg Ile Leu

85										90					95				
Leu	Lys	Glu	Lys	Met	Glu	Pro	Val	Gln	Gln	Leu	Glu	Leu	Ile	His	Asp				
			100					105					110						
Leu	Lys	Tyr	Leu	Gly	Leu	Ser	Asp	Phe	Phe	Gln	Asp	Glu	Ile	Lys	Glu				
		115					120					125							
Ile	Leu	Gly	Val	Ile	Tyr	Asn	Glu	His	Lys	Cys	Phe	His	Asn	Asn	Glu				
	130					135					140								
Val	Glu	Lys	Met	Asp	Leu	Tyr	Phe	Thr	Ala	Leu	Gly	Phe	Arg	Leu	Leu				
145					150					155					160				
Arg	Gln	His	Gly	Phe	Asn	Ile	Ser	Gln	Asp	Val	Phe	Asn	Cys	Phe	Lys				
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Asn	Glu	Lys	Gly	Ile	Asp	Phe	Lys	Ala	Ser	Leu	Ala	Gln	Asp	Thr	Lys				
			180					185					190						
Gly	Met	Leu	Gln	Leu	Tyr	Glu	Ala	Ser	Phe	Leu	Leu	Arg	Lys	Gly	Glu				
	195						200					205							
Asp	Thr	Leu	Glu	Leu	Ala	Arg	Glu	Phe	Ala	Thr	Lys	Cys	Leu	Gln	Lys				
	210					215					220								
Lys	Leu	Asp	Glu	Gly	Gly	Asn	Glu	Ile	Asp	Glu	Asn	Leu	Leu	Leu	Trp				
225				230						235					240				
Ile	Arg	His	Ser	Leu	Asp	Leu	Pro	Leu	His	Trp	Arg	Ile	Gln	Ser	Val				
			245					250						255					
Glu	Ala	Arg	Trp	Phe	Ile	Asp	Ala	Tyr	Ala	Arg	Arg	Pro	Asp	Met	Asn				
		260					265						270						
Pro	Leu	Ile	Phe	Glu	Leu	Ala	Lys	Leu	Asn	Phe	Asn	Ile	Ile	Gln	Ala				
		275					280					285							
Thr	His	Gln	Gln	Glu	Leu	Lys	Asp	Leu	Ser	Arg	Trp	Trp	Ser	Arg	Leu				
	290					295					300								
Cys	Phe	Pro	Glu	Lys	Leu	Pro	Phe	Val	Arg	Asp	Arg	Leu	Val	Glu	Ser				
305				310						315					320				
Phe	Phe	Trp	Ala	Val	Gly	Met	Phe	Glu	Pro	His	Gln	His	Gly	Tyr	Gln				
			325					330					335						
Arg	Lys	Met	Ala	Ala	Thr	Ile	Ile	Val	Leu	Ala	Thr	Val	Ile	Asp	Asp				
			340					345					350						
Ile	Tyr	Asp	Val	Tyr	Gly	Thr	Leu	Asp	Glu	Leu	Glu	Leu	Phe	Thr	Asp				
	355						360					365							
Thr	Phe	Lys	Arg	Trp	Asp	Thr	Glu	Ser	Ile	Thr	Arg	Leu	Pro	Tyr	Tyr				
	370				375						380								
Met	Gln	Leu	Cys	Tyr	Trp	Gly	Val	His	Asn	Tyr	Ile	Ser	Asp	Ala	Ala				
385					390					395					400				
Tyr	Asp	Ile	Leu	Lys	Glu	His	Gly	Phe	Phe	Cys	Leu	Gln	Tyr	Leu	Arg				

405										410				415			
Lys	Ser	Val	Val	Asp	Leu	Val	Glu	Ala	Tyr	Phe	His	Glu	Ala	Lys	Trp		
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Tyr	His	Ser	Gly	Tyr	Thr	Pro	Ser	Leu	Asp	Glu	Tyr	Leu	Asn	Ile	Ala		
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Lys	Ile	Ser	Val	Ala	Ser	Pro	Ala	Ile	Ile	Ser	Pro	Thr	Tyr	Phe	Thr		
	450					455					460						
Phe	Ala	Asn	Ala	Ser	His	Asp	Thr	Ala	Val	Ile	Asp	Ser	Leu	Tyr	Gln		
465					470					475					480		
Tyr	His	Asp	Ile	Leu	Cys	Leu	Ala	Gly	Ile	Ile	Leu	Arg	Leu	Pro	Asp		
				485					490					495			
Asp	Leu	Gly	Thr	Ser	Tyr	Phe	Glu	Leu	Ala	Arg	Gly	Asp	Val	Pro	Lys		
			500					505					510				
Thr	Ile	Gln	Cys	Tyr	Met	Lys	Glu	Thr	Asn	Ala	Ser	Glu	Glu	Glu	Ala		
		515					520					525					
Val	Glu	His	Val	Lys	Phe	Leu	Ile	Arg	Glu	Ala	Trp	Lys	Asp	Met	Asn		
	530					535					540						
Thr	Ala	Ile	Ala	Ala	Gly	Tyr	Pro	Phe	Pro	Asp	Gly	Met	Val	Ala	Gly		
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Ala	Ala	Asn	Ile	Gly	Arg	Val	Ala	Gln	Phe	Ile	Tyr	Leu	His	Gly	Asp		
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Gly	Phe	Gly	Val	Gln	His	Ser	Lys	Thr	Tyr	Glu	His	Ile	Ala	Gly	Leu		
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<210> 35
<211> 598
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:
computer-generated protein sequence

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<220>
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<222> (1)..(598)
<223> Computer-generated (+)-bornyl diphosphate synthase
sequence variant
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Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser Ser Lys Leu
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 Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln Pro Ala Leu
 50 55 60
 Trp Asp Ser Asn Tyr Leu Gln Ser Leu Asn Thr Pro Tyr Thr Glu Glu
 65 70 75 80
 Arg His Leu Asp Arg Lys Ala Glu Leu Ile Val Gln Val Arg Ile Leu
 85 90 95
 Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu Ile His Asp
 100 105 110
 Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu Ile Lys Glu
 115 120 125
 Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His Asn Asn Glu
 130 135 140
 Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Leu Leu
 145 150 155 160
 Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn Cys Phe Lys
 165 170 175
 Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln Asp Thr Lys
 180 185 190
 Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Lys Gly Glu
 195 200 205
 Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys Leu Gln Lys
 210 215 220
 Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu Leu Leu Trp
 225 230 235 240
 Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile Gln Ser Val
 245 250 255
 Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn
 260 265 270
 Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile Ile Gln Ala
 275 280 285
 Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu
 290 295 300
 Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser
 305 310 315 320
 Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln
 325 330 335
 Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp
 340 345 350

Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu Phe Thr Asp
 355 360 365
 Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu Pro Tyr Tyr
 370 375 380
 Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser Asp Ala Ala
 385 390 395 400
 Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln Tyr Leu Arg
 405 410 415
 Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu Ala Lys Trp
 420 425 430
 Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu Asn Ile Ala
 435 440 445
 Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr Tyr Phe Thr
 450 455 460
 Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser Leu Tyr Gln
 465 470 475 480
 Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg Leu Pro Asp
 485 490 495
 Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp Val Pro Lys
 500 505 510
 Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu Glu Glu Ala
 515 520 525
 Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Asp Met Asn
 530 535 540
 Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly
 545 550 555 560
 Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu His Gly Asp
 565 570 575
 Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile Ala Gly Leu
 580 585 590
 Leu Phe Glu Pro Tyr Ala
 595

<210> 36

<211> 598

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 computer-generated protein sequence

<220>

<221> VARIANT

<222> (1)..(598)

<223> Computer-generated (+)-bornyl diphosphate synthase
protein sequence variant

<400> 36

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Met Ser Ile Ile Ser Met Asn Val Ser Ile Leu Ser Lys Pro Leu Asn
 1           5           10           15

Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu Leu Val Pro
      20           25           30

Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser Ser Lys Leu
      35           40           45

Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln Pro Ala Leu
      50           55           60

Trp Asp Ser Asn Tyr Ile Gln Ser Ile Asn Thr Pro Tyr Thr Glu Glu
 65           70           75           80

Arg His Leu Asp Arg Lys Ala Glu Leu Ile Val Gln Val Arg Ile Leu
      85           90           95

Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu Ile His Asp
      100          105          110

Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu Ile Lys Glu
      115          120          125

Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His Asn Asn Glu
      130          135          140

Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Leu Leu
      145          150          155          160

Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn Cys Phe Lys
      165          170          175

Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln Asp Thr Lys
      180          185          190

Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Lys Gly Glu
      195          200          205

Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys Leu Gln Lys
      210          215          220

Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu Leu Leu Trp
      225          230          235          240

Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile Gln Ser Val
      245          250          255

Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn
      260          265          270

Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile Ile Gln Ala
      275          280          285

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Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu
 290 295 300
 Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser
 305 310 315 320
 Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln
 325 330 335
 Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp
 340 345 350
 Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu Phe Thr Asp
 355 360 365
 Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu Pro Tyr Tyr
 370 375 380
 Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser Asp Ala Ala
 385 390 395 400
 Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln Tyr Leu Arg
 405 410 415
 Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu Ala Lys Trp
 420 425 430
 Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu Asn Ile Ala
 435 440 445
 Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr Tyr Phe Thr
 450 455 460
 Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser Leu Tyr Gln
 465 470 475 480
 Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg Leu Pro Asp
 485 490 495
 Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp Val Pro Lys
 500 505 510
 Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu Glu Glu Ala
 515 520 525
 Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Asp Met Asn
 530 535 540
 Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly
 545 550 555 560
 Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu His Gly Asp
 565 570 575
 Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile Ala Gly Leu
 580 585 590
 Leu Phe Glu Pro Tyr Ala
 595

<210> 37
 <211> 598
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 computer-generated sequence variant

<220>
 <221> VARIANT
 <222> (1)..(598)
 <223> Computer-generated (+)-bornyl diphosphate synthase
 protein variant

<400> 37
 Met Ser Ile Ile Ser Met Asn Val Ser Ile Leu Ser Lys Pro Leu Asn
 1 5 10 15
 Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu Leu Val Pro
 20 25 30
 Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser Ser Lys Leu
 35 40 45
 Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln Pro Ala Leu
 50 55 60
 Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Thr Glu Glu
 65 70 75 80
 Arg His Val Asp Arg Lys Ala Glu Leu Ile Val Gln Val Arg Ile Leu
 85 90 95
 Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu Ile His Asp
 100 105 110
 Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu Ile Lys Glu
 115 120 125
 Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His Asn Asn Glu
 130 135 140
 Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Leu Leu
 145 150 155 160
 Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn Cys Phe Lys
 165 170 175
 Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln Asp Thr Lys
 180 185 190
 Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Lys Gly Glu
 195 200 205
 Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys Leu Gln Lys
 210 215 220
 Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu Leu Leu Trp

225	230	235	240
Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile Gln Ser Val	245	250	255
Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn	260	265	270
Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile Ile Gln Ala	275	280	285
Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu	290	295	300
Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser	305	310	315
Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln	320	325	330
Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp	335	340	345
Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu Phe Thr Asp	350	355	360
Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu Pro Tyr Tyr	365	370	375
Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser Asp Ala Ala	380	385	390
Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln Tyr Leu Arg	395	400	405
Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu Ala Lys Trp	410	415	420
Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu Asn Ile Ala	425	430	435
Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr Tyr Phe Thr	440	445	450
Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser Leu Tyr Gln	455	460	465
Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg Leu Pro Asp	470	475	480
Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp Val Pro Lys	485	490	495
Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu Glu Glu Ala	500	505	510
Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Asp Met Asn	515	520	525
Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly	530	535	540

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<210> 38
<211> 598
<212> PRT
<213> Artificial Sequence
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<220>
<221> VARIANT
<222> (1)..(598)
<223> Computer-generated (+)-bornyl diphosphate synthase
      protein sequence variant

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- 73 -

Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln Asp Thr Lys
 180 185 190
 Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Lys Gly Glu
 195 200 205
 Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys Leu Gln Lys
 210 215 220
 Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu Leu Leu Trp
 225 230 235 240
 Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile Gln Ser Val
 245 250 255
 Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn
 260 265 270
 Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile Ile Gln Ala
 275 280 285
 Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu
 290 295 300
 Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser
 305 310 315 320
 Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln
 325 330 335
 Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp
 340 345 350
 Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu Phe Thr Asp
 355 360 365
 Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu Pro Tyr Tyr
 370 375 380
 Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser Asp Ala Ala
 385 390 395 400
 Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln Tyr Leu Arg
 405 410 415
 Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu Ala Lys Trp
 420 425 430
 Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu Asn Ile Ala
 435 440 445
 Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr Tyr Phe Thr
 450 455 460
 Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser Leu Tyr Gln
 465 470 475 480
 Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg Leu Pro Asp
 485 490 495

Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp Val Pro Lys
 500 505 510
 Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu Glu Glu Ala
 515 520 525
 Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Asp Met Asn
 530 535 540
 Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly
 545 550 555 560
 Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu His Gly Asp
 565 570 575
 Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile Ala Gly Leu
 580 585 590
 Leu Phe Glu Pro Tyr Ala
 595

<210> 39
 <211> 598
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 computer-generated sequence variant

<220>
 <221> VARIANT
 <222> (1)..(598)
 <223> computer-generated (+)-bornyl diphosphate synthase
 protein sequence variant

<400> 39
 Met Ser Ile Ile Ser Met Asn Val Ser Ile Leu Ser Lys Pro Leu Asn
 1 5 10 15
 Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu Leu Val Pro
 20 25 30
 Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser Ser Lys Leu
 35 40 45
 Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln Pro Ala Leu
 50 55 60
 Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Thr Glu Glu
 65 70 75 80
 Arg His Leu Asp Arg Lys Ala Glu Leu Ile Leu Gln Val Arg Ile Leu
 85 90 95
 Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu Ile His Asp
 100 105 110

Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu Ile Lys Glu
 115 120 125
 Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His Asn Asn Glu
 130 135 140
 Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Leu Leu
 145 150 155 160
 Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn Cys Phe Lys
 165 170 175
 Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln Asp Thr Lys
 180 185 190
 Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Lys Gly Glu
 195 200 205
 Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys Leu Gln Lys
 210 215 220
 Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu Leu Leu Trp
 225 230 235 240
 Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile Gln Ser Val
 245 250 255
 Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn
 260 265 270
 Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile Ile Gln Ala
 275 280 285
 Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu
 290 295 300
 Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser
 305 310 315 320
 Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln
 325 330 335
 Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp
 340 345 350
 Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu Phe Thr Asp
 355 360 365
 Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu Pro Tyr Tyr
 370 375 380
 Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser Asp Ala Ala
 385 390 395 400
 Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln Tyr Leu Arg
 405 410 415
 Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu Ala Lys Trp
 420 425 430

Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu Asn Ile Ala
 435 440 445
 Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr Tyr Phe Thr
 450 455 460
 Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser Leu Tyr Gln
 465 470 475 480
 Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg Leu Pro Asp
 485 490 495
 Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp Val Pro Lys
 500 505 510
 Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu Glu Glu Ala
 515 520 525
 Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Asp Met Asn
 530 535 540
 Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly
 545 550 555 560
 Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu His Gly Asp
 565 570 575
 Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile Ala Gly Leu
 580 585 590
 Leu Phe Glu Pro Tyr Ala
 595

<210> 40

<211> 598

<212> PRT

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:
 computer-generated sequence variant

<220>

<221> VARIANT

<222> (1)..(598)

 <223> computer-generated (+)-bornyl diphosphate synthase
 protein sequence variant

<400> 40

Met Ser Ile Ile Ser Met Asn Val Ser Ile Leu Ser Lys Pro Leu Asn
 1 5 10 15
 Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu Leu Val Pro
 20 25 30
 Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser Ser Lys Leu
 35 40 45
 Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln Pro Ala Leu

50	55	60
Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Thr Glu Glu 65 70 75 80		
Arg His Leu Asp Arg Lys Ala Glu Leu Ile Val Gln Val Arg Leu Leu 85 90 95		
Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu Ile His Asp 100 105 110		
Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu Ile Lys Glu 115 120 125		
Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His Asn Asn Glu 130 135 140		
Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Leu Leu 145 150 155 160		
Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn Cys Phe Lys 165 170 175		
Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln Asp Thr Lys 180 185 190		
Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Lys Gly Glu 195 200 205		
Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys Leu Gln Lys 210 215 220		
Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu Leu Leu Trp 225 230 235 240		
Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile Gln Ser Val 245 250 255		
Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn 260 265 270		
Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile Ile Gln Ala 275 280 285		
Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu 290 295 300		
Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser 305 310 315 320		
Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln 325 330 335		
Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp 340 345 350		
Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu Phe Thr Asp 355 360 365		
Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu Pro Tyr Tyr		

370 375 380
 Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser Asp Ala Ala
 385 390 395 400
 Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln Tyr Leu Arg
 405 410 415
 Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu Ala Lys Trp
 420 425 430
 Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu Asn Ile Ala
 435 440 445
 Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr Tyr Phe Thr
 450 455 460
 Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser Leu Tyr Gln
 465 470 475 480
 Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg Leu Pro Asp
 485 490 495
 Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp Val Pro Lys
 500 505 510
 Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu Glu Glu Ala
 515 520 525
 Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Asp Met Asn
 530 535 540
 Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly
 545 550 555 560
 Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu His Gly Asp
 565 570 575
 Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile Ala Gly Leu
 580 585 590
 Leu Phe Glu Pro Tyr Ala
 595

<210> 41

<211> 598

<212> PRT

<213> Artificial Sequence

<220>

 <223> Description of Artificial
 Sequence: computer-generated protein sequence

<220>

<221> VARIANT

<222> (1)..(598)

 <223> computer-generated (+)-bornyl diphosphate synthase
 protein sequence variant

<400> 41
Met Ser Ile Ile Ser Met Asn Val Ser Ile Leu Ser Lys Pro Leu Asn
1 5 10 15
Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu Leu Val Pro
20 25 30
Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser Ser Lys Leu
35 40 45
Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln Pro Ala Leu
50 55 60
Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Thr Glu Glu
65 70 75 80
Arg His Leu Asp Arg Lys Ala Glu Leu Ile Val Gln Val Arg Ile Val
85 90 95
Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu Ile His Asp
100 105 110
Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu Ile Lys Glu
115 120 125
Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His Asn Asn Glu
130 135 140
Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Leu Leu
145 150 155 160
Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn Cys Phe Lys
165 170 175
Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln Asp Thr Lys
180 185 190
Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Lys Gly Glu
195 200 205
Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys Leu Gln Lys
210 215 220
Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu Leu Leu Trp
225 230 235 240
Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile Gln Ser Val
245 250 255
Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn
260 265 270
Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile Ile Gln Ala
275 280 285
Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu
290 295 300
Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser
305 310 315 320

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<210> 42
<211> 598
<212> PRT
<213> Artificial Sequence
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<220>

<223> Description of Artificial Sequence:
computer-generated protein sequence

<220>

<221> VARIANT

<222> (1)..(598)

<223> computer-generated (+)-bornyl diphosphate synthase
protein sequence variant

<400> 42

Met	Ser	Ile	Ile	Ser	Met	Asn	Val	Ser	Ile	Leu	Ser	Lys	Pro	Leu	Asn	1	5	10	15
Cys	Leu	His	Asn	Leu	Glu	Arg	Arg	Pro	Ser	Lys	Ala	Leu	Leu	Val	Pro	20	25	30	
Cys	Thr	Ala	Pro	Thr	Ala	Arg	Leu	Arg	Ala	Ser	Cys	Ser	Ser	Lys	Leu	35	40	45	
Gln	Glu	Ala	His	Gln	Ile	Arg	Arg	Ser	Gly	Asn	Tyr	Gln	Pro	Ala	Leu	50	55	60	
Trp	Asp	Ser	Asn	Tyr	Ile	Gln	Ser	Leu	Asn	Thr	Pro	Tyr	Thr	Glu	Glu	65	70	75	80
Arg	His	Leu	Asp	Arg	Lys	Ala	Glu	Leu	Ile	Val	Gln	Val	Arg	Ile	Leu	85	90	95	
Ile	Lys	Glu	Lys	Met	Glu	Pro	Val	Gln	Gln	Leu	Glu	Leu	Ile	His	Asp	100	105	110	
Leu	Lys	Tyr	Leu	Gly	Leu	Ser	Asp	Phe	Phe	Gln	Asp	Glu	Ile	Lys	Glu	115	120	125	
Ile	Leu	Gly	Val	Ile	Tyr	Asn	Glu	His	Lys	Cys	Phe	His	Asn	Asn	Glu	130	135	140	
Val	Glu	Lys	Met	Asp	Leu	Tyr	Phe	Thr	Ala	Leu	Gly	Phe	Arg	Leu	Leu	145	150	155	160
Arg	Gln	His	Gly	Phe	Asn	Ile	Ser	Gln	Asp	Val	Phe	Asn	Cys	Phe	Lys	165	170	175	
Asn	Glu	Lys	Gly	Ile	Asp	Phe	Lys	Ala	Ser	Leu	Ala	Gln	Asp	Thr	Lys	180	185	190	
Gly	Met	Leu	Gln	Leu	Tyr	Glu	Ala	Ser	Phe	Leu	Leu	Arg	Lys	Gly	Glu	195	200	205	
Asp	Thr	Leu	Glu	Leu	Ala	Arg	Glu	Phe	Ala	Thr	Lys	Cys	Leu	Gln	Lys	210	215	220	
Lys	Leu	Asp	Glu	Gly	Gly	Asn	Glu	Ile	Asp	Glu	Asn	Leu	Leu	Leu	Trp	225	230	235	240
Ile	Arg	His	Ser	Leu	Asp	Leu	Pro	Leu	His	Trp	Arg	Ile	Gln	Ser	Val	245	250	255	

Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn
 260 265 270
 Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile Ile Gln Ala
 275 280 285
 Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu
 290 295 300
 Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser
 305 310 315 320
 Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln
 325 330 335
 Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp
 340 345 350
 Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu Phe Thr Asp
 355 360 365
 Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu Pro Tyr Tyr
 370 375 380
 Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser Asp Ala Ala
 385 390 395 400
 Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln Tyr Leu Arg
 405 410 415
 Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu Ala Lys Trp
 420 425 430
 Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu Asn Ile Ala
 435 440 445
 Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr Tyr Phe Thr
 450 455 460
 Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser Leu Tyr Gln
 465 470 475 480
 Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg Leu Pro Asp
 485 490 495
 Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp Val Pro Lys
 500 505 510
 Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu Glu Glu Ala
 515 520 525
 Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Asp Met Asn
 530 535 540
 Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly
 545 550 555 560
 Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu His Gly Asp
 565 570 575

Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile Ala Gly Leu
580 585 590

Leu Phe Glu Pro Tyr Ala
595

<210> 43

<211> 1912

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
computer-generated nucleic acid sequence

<220>

<221> CDS

<222> (26)..(1792)

<223> computer-generated nucleic acid sequence encoding
(+)-sabinene synthase

<400> 43

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                        1 5

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Met Pro Leu Asn Ser Leu His Asn Phe Glu Arg Lys Pro Ser Lys Ala
10 15 20 25

tgg tct acc tct tgc act gca ccc gca gct cgc ctc egg gca tct tcc 148
Trp Ser Thr Ser Cys Thr Ala Pro Ala Ala Arg Leu Arg Ala Ser Ser
30 35 40

tct tta caa caa gaa aaa cct cac caa atc cga cgc tct ggg gat tac 196
Ser Leu Gln Gln Glu Lys Pro His Gln Ile Arg Arg Ser Gly Asp Tyr
45 50 55

caa ccc tct att tgg gat ttc aat tac ata cag tct ctc aac act ccg 244
Gln Pro Ser Ile Trp Asp Phe Asn Tyr Ile Gln Ser Leu Asn Thr Pro
60 65 70

tat aag gag cag aga cac ttt aat agg caa gca gag ttg att atg caa 292
Tyr Lys Glu Gln Arg His Phe Asn Arg Gln Ala Glu Leu Ile Met Gln
75 80 85

gtg agg atg ttg ctc aag gta aag atg gag gca att caa cag ttg gag 340
Val Arg Met Leu Leu Lys Val Lys Met Glu Ala Ile Gln Gln Leu Glu
90 95 100 105

ttg att gat gac ttg caa tac ctg gga ctg tct tat ttc ttt caa gat 388
Leu Ile Asp Asp Leu Gln Tyr Leu Gly Leu Ser Tyr Phe Phe Gln Asp
110 115 120

gag att aaa caa atc tta agt tct ata cac aat gag ccc aga tat ttc 436
Glu Ile Lys Gln Ile Leu Ser Ser Ile His Asn Glu Pro Arg Tyr Phe
125 130 135

cac aat aat gat ttg tat ttc aca gct ctt gga ttc aga atc ctc aga 484

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His	Asn	Asn	Asp	Leu	Tyr	Phe	Thr	Ala	Leu	Gly	Phe	Arg	Ile	Leu	Arg	
	140						145					150				
caa	cat	ggt	ttt	aat	gtt	tcc	gaa	gat	gta	ttt	gat	tgt	ttc	aaa	att	532
Gln	His	Gly	Phe	Asn	Val	Ser	Glu	Asp	Val	Phe	Asp	Cys	Phe	Lys	Ile	
	155					160				165						
gag	aag	tgc	agt	gat	ttc	aat	gca	aac	ctt	gct	caa	gat	acg	aag	gga	580
Glu	Lys	Cys	Ser	Asp	Phe	Asn	Ala	Asn	Leu	Ala	Gln	Asp	Thr	Lys	Gly	
	170				175				180						185	
atg	tta	caa	ctt	tat	gaa	gca	tct	ttc	ctt	ttg	aga	gaa	ggt	gaa	gat	628
Met	Leu	Gln	Leu	Tyr	Glu	Ala	Ser	Phe	Leu	Leu	Arg	Glu	Gly	Glu	Asp	
				190					195					200		
aca	ttg	gag	cta	gca	aga	cga	ttt	tcc	acc	aga	tct	cta	cga	gaa	aaa	676
Thr	Leu	Glu	Leu	Ala	Arg	Arg	Phe	Ser	Thr	Arg	Ser	Leu	Arg	Glu	Lys	
			205					210					215			
ttt	gat	gaa	ggt	ggt	gat	gaa	att	gat	gaa	gat	cta	tca	tcg	tgg	att	724
Phe	Asp	Glu	Gly	Gly	Asp	Glu	Ile	Asp	Glu	Asp	Leu	Ser	Ser	Trp	Ile	
		220					225					230				
cgc	cat	tcc	ttg	gat	ctt	cct	ctt	cat	tgg	agg	gtc	caa	gga	tta	gag	772
Arg	His	Ser	Leu	Asp	Leu	Pro	Leu	His	Trp	Arg	Val	Gln	Gly	Leu	Glu	
	235					240					245					
gca	aga	tgg	ttc	tta	gat	gct	tat	gcg	agg	agg	ccg	gac	atg	aat	cca	820
Ala	Arg	Trp	Phe	Leu	Asp	Ala	Tyr	Ala	Arg	Arg	Pro	Asp	Met	Asn	Pro	
	250				255				260						265	
ctt	att	ttc	aaa	ctc	gcc	aaa	ctc	aac	ttc	aat	att	gtt	cag	gca	aca	868
Leu	Ile	Phe	Lys	Leu	Ala	Lys	Leu	Asn	Phe	Asn	Ile	Val	Gln	Ala	Thr	
				270					275					280		
tat	caa	gaa	gaa	ctg	aaa	gat	atc	tca	agg	tgg	tgg	aat	agt	tcg	tgc	916
Tyr	Gln	Glu	Glu	Leu	Lys	Asp	Ile	Ser	Arg	Trp	Trp	Asn	Ser	Ser	Cys	
			285					290					295			
ctt	gct	gag	aaa	ctc	cca	ttt	gtg	aga	gat	agg	att	gtg	gaa	tgc	ttc	964
Leu	Ala	Glu	Lys	Leu	Pro	Phe	Val	Arg	Asp	Arg	Ile	Val	Glu	Cys	Phe	
		300					305					310				
ttt	tgg	gcc	atc	gcg	gct	ttt	gag	cct	cac	caa	tat	agt	tat	cag	aga	1012
Phe	Trp	Ala	Ile	Ala	Ala	Phe	Glu	Pro	His	Gln	Tyr	Ser	Tyr	Gln	Arg	
	315					320					325					
aaa	atg	gcc	gcc	gtt	att	att	act	ttc	ata	aca	att	atc	gat	gat	gtt	1060
Lys	Met	Ala	Ala	Val	Ile	Ile	Thr	Phe	Ile	Thr	Ile	Ile	Asp	Asp	Val	
	330				335					340					345	
tat	gat	gtg	tat	gga	aca	ata	gaa	gaa	cta	gaa	cta	tta	aca	gat	atg	1108
Tyr	Asp	Val	Tyr	Gly	Thr	Ile	Glu	Glu	Leu	Glu	Leu	Leu	Thr	Asp	Met	
				350					355					360		
att	cgc	aga	tgg	gat	aat	aaa	tca	ata	agc	caa	ctt	cca	tat	tat	atg	1156
Ile	Arg	Arg	Trp	Asp	Asn	Lys	Ser	Ile	Ser	Gln	Leu	Pro	Tyr	Tyr	Met	
			365					370					375			
caa	gtg	tgc	tat	ttg	gca	cta	tac	aac	ttc	gtt	tct	gag	cgg	gct	tac	1204

Gln Val Cys Tyr Leu Ala Leu Tyr Asn Phe Val Ser Glu Arg Ala Tyr	
380 385 390	
gat att cta aaa gat caa cat ttc aac agc atc cca tat tta cag aga	1252
Asp Ile Leu Lys Asp Gln His Phe Asn Ser Ile Pro Tyr Leu Gln Arg	
395 400 405	
tcg tgg gta agt ttg gtt gaa gga tat ctt aag gag gca tac tgg tac	1300
Ser Trp Val Ser Leu Val Glu Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr	
410 415 420 425	
tac aat ggc tat aaa cca agc ttg gaa gaa tat ctc aac aac gcc aag	1348
Tyr Asn Gly Tyr Lys Pro Ser Leu Glu Glu Tyr Leu Asn Asn Ala Lys	
430 435 440	
att tca ata tcg gct cct aca atc ata tcc cag ctt tat ttt aca tta	1396
Ile Ser Ile Ser Ala Pro Thr Ile Ile Ser Gln Leu Tyr Phe Thr Leu	
445 450 455	
gca aac tcg att gat gaa aca gct atc gag agc ttg tac caa tat cat	1444
Ala Asn Ser Ile Asp Glu Thr Ala Ile Glu Ser Leu Tyr Gln Tyr His	
460 465 470	
aac ata ctt tac cta tca gga acc ata tta agg ctt gct gac gat ctt	1492
Asn Ile Leu Tyr Leu Ser Gly Thr Ile Leu Arg Leu Ala Asp Asp Leu	
475 480 485	
ggg aca tca caa cat gag ctg gag aga gga gac gta ccg aaa gca atc	1540
Gly Thr Ser Gln His Glu Leu Glu Arg Gly Asp Val Pro Lys Ala Ile	
490 495 500 505	
cag tgc tac atg aat gac aca aat gct tcg gag aga gag gcg gtg gaa	1588
Gln Cys Tyr Met Asn Asp Thr Asn Ala Ser Glu Arg Glu Ala Val Glu	
510 515 520	
cac gtg aag ttt ctg ata agg gag gcg tgg aag gag atg aac acg gtc	1636
His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Glu Met Asn Thr Val	
525 530 535	
aca aca gcc agc gat tgt ccg ttt acg gat gat ttg gtt gcg gcc gca	1684
Thr Thr Ala Ser Asp Cys Pro Phe Thr Asp Asp Leu Val Ala Ala Ala	
540 545 550	
gct aat ctt gca agg gcg gct cag ttt ata tat ctc gac ggg gat ggg	1732
Ala Asn Leu Ala Arg Ala Ala Gln Phe Ile Tyr Leu Asp Gly Asp Gly	
555 560 565	
cat ggc gtg caa cac tca gaa ata cat caa cag atg gga ggc ctg cta	1780
His Gly Val Gln His Ser Glu Ile His Gln Gln Met Gly Gly Leu Leu	
570 575 580 585	
ttc cag cct tat gtctgaataa atcgaaaatc caacctacta tgtatccctc	1832
Phe Gln Pro Tyr	
gataatatat tcttgggggtt aacatgttta attaaagttc taatttaaag agctgaatcg	1892
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<210> 44

<211> 589

<212> PRT

<213> Artificial Sequence

<400> 44

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Pro Ala Ala Arg Leu Arg Ala Ser Ser Ser Leu Gln Gln Glu Lys Pro
      35           40           45

His Gln Ile Arg Arg Ser Gly Asp Tyr Gln Pro Ser Ile Trp Asp Phe
      50           55           60

Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Lys Glu Gln Arg His Phe
      65           70           75           80

Asn Arg Gln Ala Glu Leu Ile Met Gln Val Arg Met Leu Leu Lys Val
      85           90           95

Lys Met Glu Ala Ile Gln Gln Leu Glu Leu Ile Asp Asp Leu Gln Tyr
      100          105          110

Leu Gly Leu Ser Tyr Phe Phe Gln Asp Glu Ile Lys Gln Ile Leu Ser
      115          120          125

Ser Ile His Asn Glu Pro Arg Tyr Phe His Asn Asn Asp Leu Tyr Phe
      130          135          140

Thr Ala Leu Gly Phe Arg Ile Leu Arg Gln His Gly Phe Asn Val Ser
      145          150          155          160

Glu Asp Val Phe Asp Cys Phe Lys Ile Glu Lys Cys Ser Asp Phe Asn
      165          170          175

Ala Asn Leu Ala Gln Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala
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Ser Phe Leu Leu Arg Glu Gly Glu Asp Thr Leu Glu Leu Ala Arg Arg
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Phe Ser Thr Arg Ser Leu Arg Glu Lys Phe Asp Glu Gly Gly Asp Glu
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Ile Asp Glu Asp Leu Ser Ser Trp Ile Arg His Ser Leu Asp Leu Pro
      225          230          235          240

Leu His Trp Arg Val Gln Gly Leu Glu Ala Arg Trp Phe Leu Asp Ala
      245          250          255

Tyr Ala Arg Arg Pro Asp Met Asn Pro Leu Ile Phe Lys Leu Ala Lys
      260          265          270

Leu Asn Phe Asn Ile Val Gln Ala Thr Tyr Gln Glu Glu Leu Lys Asp
      275          280          285

Ile Ser Arg Trp Trp Asn Ser Ser Cys Leu Ala Glu Lys Leu Pro Phe

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290					295					300					
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Glu	Pro	His	Gln	Tyr 325	Ser	Tyr	Gln	Arg	Lys 330	Met	Ala	Ala	Val	Ile 335	Ile
Thr	Phe	Ile	Thr 340	Ile	Ile	Asp	Asp	Val 345	Tyr	Asp	Val	Tyr	Gly 350	Thr	Ile
Glu	Glu	Leu 355	Glu	Leu	Leu	Thr	Asp 360	Met	Ile	Arg	Arg	Trp 365	Asp	Asn	Lys
Ser 370	Ile	Ser	Gln	Leu	Pro	Tyr 375	Tyr	Met	Gln	Val	Cys 380	Tyr	Leu	Ala	Leu
Tyr 385	Asn	Phe	Val	Ser	Glu 390	Arg	Ala	Tyr	Asp	Ile 395	Leu	Lys	Asp	Gln	His 400
Phe	Asn	Ser	Ile	Pro 405	Tyr	Leu	Gln	Arg	Ser 410	Trp	Val	Ser	Leu	Val 415	Glu
Gly	Tyr	Leu	Lys 420	Glu	Ala	Tyr	Trp	Tyr 425	Tyr	Asn	Gly	Tyr	Lys 430	Pro	Ser
Leu	Glu	Glu 435	Tyr	Leu	Asn	Asn	Ala 440	Lys	Ile	Ser	Ile	Ser 445	Ala	Pro	Thr
Ile 450	Ile	Ser	Gln	Leu	Tyr	Phe 455	Thr	Leu	Ala	Asn	Ser 460	Ile	Asp	Glu	Thr
Ala 465	Ile	Glu	Ser	Leu	Tyr 470	Gln	Tyr	His	Asn	Ile 475	Leu	Tyr	Leu	Ser	Gly 480
Thr	Ile	Leu	Arg	Leu 485	Ala	Asp	Asp	Leu	Gly 490	Thr	Ser	Gln	His	Glu 495	Leu
Glu	Arg	Gly	Asp 500	Val	Pro	Lys	Ala	Ile 505	Gln	Cys	Tyr	Met	Asn 510	Asp	Thr
Asn	Ala	Ser 515	Glu	Arg	Glu	Ala	Val 520	Glu	His	Val	Lys	Phe 525	Leu	Ile	Arg
Glu 530	Ala	Trp	Lys	Glu	Met	Asn 535	Thr	Val	Thr	Thr	Ala 540	Ser	Asp	Cys	Pro
Phe 545	Thr	Asp	Asp	Leu	Val 550	Ala	Ala	Ala	Ala	Asn 555	Leu	Ala	Arg	Ala	Ala 560
Gln	Phe	Ile	Tyr	Leu 565	Asp	Gly	Asp	Gly	His 570	Gly	Val	Gln	His	Ser 575	Glu
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<210> 45

<211> 1912

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
computer-generated nucleic acid sequence

<220>

<221> CDS

<222> (26) .. (1792)

<223> computer-generated nucleic acid sequence encoding
(+)-sabinene synthase

<400> 45

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Met Pro Leu Asn Ser Leu His Asn Phe Glu Arg Lys Pro Ser Lys Ala	
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tgg tct acc tct tgc act gca ccc gca gct cgc ctc cgg gca tct tcc	148
Trp Ser Thr Ser Cys Thr Ala Pro Ala Ala Arg Leu Arg Ala Ser Ser	
30 35 40	
tcc tta caa caa gaa aaa cct cac caa atc cga cgc tct ggg gat tac	196
Ser Leu Gln Gln Glu Lys Pro His Gln Ile Arg Arg Ser Gly Asp Tyr	
45 50 55	
caa ccc tct ctt tgg gat ttc aat tac gta cag tct ctc aac act ccg	244
Gln Pro Ser Leu Trp Asp Phe Asn Tyr Val Gln Ser Leu Asn Thr Pro	
60 65 70	
tat aag gag cag aga cac ttt aat agg caa gca gag ttg att atg caa	292
Tyr Lys Glu Gln Arg His Phe Asn Arg Gln Ala Glu Leu Ile Met Gln	
75 80 85	
gtg agg atg ttg ctc aag gta aag atg gag gca att caa cag ttg gag	340
Val Arg Met Leu Leu Lys Val Lys Met Glu Ala Ile Gln Gln Leu Glu	
90 95 100 105	
ttg att gat gac ttg caa tac ctg gga ctg tct tat ttc ttt caa gat	388
Leu Ile Asp Asp Leu Gln Tyr Leu Gly Leu Ser Tyr Phe Phe Gln Asp	
110 115 120	
gag att aaa caa atc tta agt tct ata cac aat gag ccc aga tat ttc	436
Glu Ile Lys Gln Ile Leu Ser Ser Ile His Asn Glu Pro Arg Tyr Phe	
125 130 135	
cac aat aat gat ttg tat ttc aca gct ctt gga ttc aga atc ctc aga	484
His Asn Asn Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Ile Leu Arg	
140 145 150	
caa cat ggt ttt aat gtt tcc gaa gat gta ttt gat tgt ttc aaa att	532
Gln His Gly Phe Asn Val Ser Glu Asp Val Phe Asp Cys Phe Lys Ile	
155 160 165	
gag aag tgc agt gat ttc aat gca aac ctt gct caa gat acg aag gga	580
Glu Lys Cys Ser Asp Phe Asn Ala Asn Leu Ala Gln Asp Thr Lys Gly	
170 175 180 185	

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ttt gat gaa ggt ggt gat gaa att gat gaa gat cta tca tcg tgg att Phe Asp Glu Gly Gly Asp Glu Ile Asp Glu Asp Leu Ser Ser Trp Ile 220 225 230	724
cgc cat tcc ttg gat ctt cct ctt cat tgg agg gtc caa gga tta gag Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Val Gln Gly Leu Glu 235 240 245	772
gca aga tgg ttc tta gat gct tat gcg agg agg ccg gac atg aat cca Ala Arg Trp Phe Leu Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn Pro 250 255 260 265	820
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aaa atg gcc gcc gtt att att act ttc ata aca att atc gat gat gtt Lys Met Ala Ala Val Ile Ile Thr Phe Ile Thr Ile Ile Asp Asp Val 330 335 340 345	1060
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att cgc aga tgg gat aat aaa tca ata agc caa ctt cca tat tat atg Ile Arg Arg Trp Asp Asn Lys Ser Ile Ser Gln Leu Pro Tyr Tyr Met 365 370 375	1156
caa gtg tgc tat ttg gca cta tac aac ttc gtt tct gag cgg gct tac Gln Val Cys Tyr Leu Ala Leu Tyr Asn Phe Val Ser Glu Arg Ala Tyr 380 385 390	1204
gat att cta aaa gat caa cat ttc aac agc atc cca tat tta cag aga Asp Ile Leu Lys Asp Gln His Phe Asn Ser Ile Pro Tyr Leu Gln Arg 395 400 405	1252
tcg tgg gta agt ttg gtt gaa gga tat ctt aag gag gca tac tgg tac Ser Trp Val Ser Leu Val Glu Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr 410 415 420 425	1300

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 Tyr Asn Gly Tyr Lys Pro Ser Leu Glu Glu Tyr Leu Asn Asn Ala Lys
 430 435 440
 att tca ata tcg gct cct aca atc ata tcc cag ctt tat ttt aca tta 1396
 Ile Ser Ile Ser Ala Pro Thr Ile Ile Ser Gln Leu Tyr Phe Thr Leu
 445 450 455
 gca aac tcg att gat gaa aca gct atc gag agc ttg tac caa tat cat 1444
 Ala Asn Ser Ile Asp Glu Thr Ala Ile Glu Ser Leu Tyr Gln Tyr His
 460 465 470
 aac ata ctt tac cta tca gga acc ata tta agg ctt gct gac gat ctt 1492
 Asn Ile Leu Tyr Leu Ser Gly Thr Ile Leu Arg Leu Ala Asp Asp Leu
 475 480 485
 ggg aca tca caa cat gag ctg gag aga gga gac gta ccg aaa gca atc 1540
 Gly Thr Ser Gln His Glu Leu Glu Arg Gly Asp Val Pro Lys Ala Ile
 490 495 500 505
 cag tgc tac atg aat gac aca aat gct tcg gag aga gag gcg gtg gaa 1588
 Gln Cys Tyr Met Asn Asp Thr Asn Ala Ser Glu Arg Glu Ala Val Glu
 510 515 520
 cac gtg aag ttt ctg ata agg gag gcg tgg aag gag atg aac acg gtc 1636
 His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Glu Met Asn Thr Val
 525 530 535
 aca aca gcc agc gat tgt ccg ttt acg gat gat ttg gtt gcg gcc gca 1684
 Thr Thr Ala Ser Asp Cys Pro Phe Thr Asp Asp Leu Val Ala Ala Ala
 540 545 550
 gct aat ctt gca agg gcg gct cag ttt ata tat ctc gac ggg gat ggg 1732
 Ala Asn Leu Ala Arg Ala Glu Phe Ile Tyr Leu Asp Gly Asp Gly
 555 560 565
 cat ggc gtg caa cac tca gaa ata cat caa cag atg gga ggc ctg cta 1780
 His Gly Val Gln His Ser Glu Ile His Gln Met Gly Gly Leu Leu
 570 575 580 585
 ttc cag cct tat gtctgaataa atcgaaaatc caacctacta tgtatccctc 1832
 Phe Gln Pro Tyr
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 atcctcaaaa aaaaaaaaaa 1912

<210> 46
 <211> 589
 <212> PRT
 <213> Artificial Sequence

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 35 40 45
 His Gln Ile Arg Arg Ser Gly Asp Tyr Gln Pro Ser Leu Trp Asp Phe
 50 55 60
 Asn Tyr Val Gln Ser Leu Asn Thr Pro Tyr Lys Glu Gln Arg His Phe
 65 70 75 80
 Asn Arg Gln Ala Glu Leu Ile Met Gln Val Arg Met Leu Leu Lys Val
 85 90 95
 Lys Met Glu Ala Ile Gln Gln Leu Glu Leu Ile Asp Asp Leu Gln Tyr
 100 105 110
 Leu Gly Leu Ser Tyr Phe Phe Gln Asp Glu Ile Lys Gln Ile Leu Ser
 115 120 125
 Ser Ile His Asn Glu Pro Arg Tyr Phe His Asn Asn Asp Leu Tyr Phe
 130 135 140
 Thr Ala Leu Gly Phe Arg Ile Leu Arg Gln His Gly Phe Asn Val Ser
 145 150 155 160
 Glu Asp Val Phe Asp Cys Phe Lys Ile Glu Lys Cys Ser Asp Phe Asn
 165 170 175
 Ala Asn Leu Ala Gln Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala
 180 185 190
 Ser Phe Leu Leu Arg Glu Gly Glu Asp Thr Leu Glu Leu Ala Arg Arg
 195 200 205
 Phe Ser Thr Arg Ser Leu Arg Glu Lys Phe Asp Glu Gly Gly Asp Glu
 210 215 220
 Ile Asp Glu Asp Leu Ser Ser Trp Ile Arg His Ser Leu Asp Leu Pro
 225 230 235 240
 Leu His Trp Arg Val Gln Gly Leu Glu Ala Arg Trp Phe Leu Asp Ala
 245 250 255
 Tyr Ala Arg Arg Pro Asp Met Asn Pro Leu Ile Phe Lys Leu Ala Lys
 260 265 270
 Leu Asn Phe Asn Ile Val Gln Ala Thr Tyr Gln Glu Glu Leu Lys Asp
 275 280 285
 Ile Ser Arg Trp Trp Asn Ser Ser Cys Leu Ala Glu Lys Leu Pro Phe
 290 295 300
 Val Arg Asp Arg Ile Val Glu Cys Phe Phe Trp Ala Ile Ala Ala Phe
 305 310 315 320
 Glu Pro His Gln Tyr Ser Tyr Gln Arg Lys Met Ala Ala Val Ile Ile
 325 330 335
 Thr Phe Ile Thr Ile Ile Asp Asp Val Tyr Asp Val Tyr Gly Thr Ile
 340 345 350

Glu Glu Leu Glu Leu Leu Thr Asp Met Ile Arg Arg Trp Asp Asn Lys
 355 360 365
 Ser Ile Ser Gln Leu Pro Tyr Tyr Met Gln Val Cys Tyr Leu Ala Leu
 370 375 380
 Tyr Asn Phe Val Ser Glu Arg Ala Tyr Asp Ile Leu Lys Asp Gln His
 385 390 395 400
 Phe Asn Ser Ile Pro Tyr Leu Gln Arg Ser Trp Val Ser Leu Val Glu
 405 410 415
 Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr Tyr Asn Gly Tyr Lys Pro Ser
 420 425 430
 Leu Glu Glu Tyr Leu Asn Asn Ala Lys Ile Ser Ile Ser Ala Pro Thr
 435 440 445
 Ile Ile Ser Gln Leu Tyr Phe Thr Leu Ala Asn Ser Ile Asp Glu Thr
 450 455 460
 Ala Ile Glu Ser Leu Tyr Gln Tyr His Asn Ile Leu Tyr Leu Ser Gly
 465 470 475 480
 Thr Ile Leu Arg Leu Ala Asp Asp Leu Gly Thr Ser Gln His Glu Leu
 485 490 495
 Glu Arg Gly Asp Val Pro Lys Ala Ile Gln Cys Tyr Met Asn Asp Thr
 500 505 510
 Asn Ala Ser Glu Arg Glu Ala Val Glu His Val Lys Phe Leu Ile Arg
 515 520 525
 Glu Ala Trp Lys Glu Met Asn Thr Val Thr Thr Ala Ser Asp Cys Pro
 530 535 540
 Phe Thr Asp Asp Leu Val Ala Ala Ala Asn Leu Ala Arg Ala Ala
 545 550 555 560
 Gln Phe Ile Tyr Leu Asp Gly Asp Gly His Gly Val Gln His Ser Glu
 565 570 575
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<211> 1912

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:
 computer-generated sequence

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<221> CDS

<222> (26)..(1792)

<223> computer-generated nucleic acid sequence encoding

(+)-sabinene synthase

<400> 47

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Met Pro Leu Asn Ser Leu His Asn Phe Glu Arg Lys Pro Ser Lys Ala
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tgg tct acc tct tgc act gca ccc gca gct cgc ctc cgg gca tct tcc 148
Trp Ser Thr Ser Cys Thr Ala Pro Ala Ala Arg Leu Arg Ala Ser Ser
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tcc tta caa caa gaa aaa cct cac caa atc cga cgc tct ggg gat tac 196
Ser Leu Gln Gln Glu Lys Pro His Gln Ile Arg Arg Ser Gly Asp Tyr
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caa ccc tct ctt tgg gat ttc aat tac ata cag tct atc aac act ccg 244
Gln Pro Ser Leu Trp Asp Phe Asn Tyr Ile Gln Ser Ile Asn Thr Pro
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tat aag gag cag aga cac ttt aat agg caa gca gag ttg att atg caa 292
Tyr Lys Glu Gln Arg His Phe Asn Arg Gln Ala Glu Leu Ile Met Gln
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gtg agg atg ttg ctc aag gta aag atg gag gca att caa cag ttg gag 340
Val Arg Met Leu Leu Lys Val Lys Met Glu Ala Ile Gln Gln Leu Glu
90                      95                      100         105

ttg att gat gac ttg caa tac ctg gga ctg tct tat ttc ttt caa gat 388
Leu Ile Asp Asp Leu Gln Tyr Leu Gly Leu Ser Tyr Phe Phe Gln Asp
                      110                     115         120

gag att aaa caa atc tta agt tct ata cac aat gag ccc aga tat ttc 436
Glu Ile Lys Gln Ile Leu Ser Ser Ile His Asn Glu Pro Arg Tyr Phe
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cac aat aat gat ttg tat ttc aca gct ctt gga ttc aga atc ctc aga 484
His Asn Asn Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Ile Leu Arg
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caa cat ggt ttt aat gtt tcc gaa gat gta ttt gat tgt ttc aaa att 532
Gln His Gly Phe Asn Val Ser Glu Asp Val Phe Asp Cys Phe Lys Ile
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gag aag tgc agt gat ttc aat gca aac ctt gct caa gat acg aag gga 580
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Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Glu Gly Glu Asp
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aca ttg gag cta gca aga cga ttt tcc acc aga tct cta cga gaa aaa 676
Thr Leu Glu Leu Ala Arg Arg Phe Ser Thr Arg Ser Leu Arg Glu Lys
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ttt gat gaa ggt ggt gat gaa att gat gaa gat cta tca tcg tgg att 724

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Arg	His	Ser	Leu	Asp	Leu	Pro	Leu	His	Trp	Arg	Val	Gln	Gly	Leu	Glu		
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Ala	Arg	Trp	Phe	Leu	Asp	Ala	Tyr	Ala	Arg	Arg	Pro	Asp	Met	Asn	Pro		
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Leu	Ile	Phe	Lys	Leu	Ala	Lys	Leu	Asn	Phe	Asn	Ile	Val	Gln	Ala	Thr		
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Tyr	Gln	Glu	Glu	Leu	Lys	Asp	Ile	Ser	Arg	Trp	Trp	Asn	Ser	Ser	Cys		
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aaa	atg	gcc	gcc	gtt	att	att	act	ttc	ata	aca	att	atc	gat	gat	gtt	1060	
Lys	Met	Ala	Ala	Val	Ile	Ile	Thr	Phe	Ile	Thr	Ile	Ile	Asp	Asp	Val		
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Tyr	Asp	Val	Tyr	Gly	Thr	Ile	Glu	Glu	Leu	Glu	Leu	Leu	Thr	Asp	Met		
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Ile	Arg	Arg	Trp	Asp	Asn	Lys	Ser	Ile	Ser	Gln	Leu	Pro	Tyr	Tyr	Met		
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caa	gtg	tgc	tat	ttg	gca	cta	tac	aac	ttc	gtt	tct	gag	cgg	gct	tac	1204	
Gln	Val	Cys	Tyr	Leu	Ala	Leu	Tyr	Asn	Phe	Val	Ser	Glu	Arg	Ala	Tyr		
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Ser	Trp	Val	Ser	Leu	Val	Glu	Gly	Tyr	Leu	Lys	Glu	Ala	Tyr	Trp	Tyr		
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tac	aat	ggc	tat	aaa	cca	agc	ttg	gaa	gaa	tat	ctc	aac	aac	gcc	aag	1348	
Tyr	Asn	Gly	Tyr	Lys	Pro	Ser	Leu	Glu	Glu	Tyr	Leu	Asn	Asn	Ala	Lys		
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Ile	Ser	Ile	Ser	Ala	Pro	Thr	Ile	Ile	Ser	Gln	Leu	Tyr	Phe	Thr	Leu		
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Ala Asn Ser Ile Asp Glu Thr Ala Ile Glu Ser Leu Tyr Gln Tyr His
 460 465 470

aac ata ctt tac cta tca gga acc ata tta agg ctt gct gac gat ctt 1492
 Asn Ile Leu Tyr Leu Ser Gly Thr Ile Leu Arg Leu Ala Asp Asp Leu
 475 480 485

ggg aca tca caa cat gag ctg gag aga gga gac gta ccg aaa gca atc 1540
 Gly Thr Ser Gln His 495 Leu Glu Arg Gly Asp Val Pro Lys Ala Ile
 490 500 505

cag tgc tac atg aat gac aca aat gct tcg gag aga gag gcg gtg gaa 1588
 Gln Cys Tyr Met Asn Asp Thr Asn Ala Ser Glu Arg Glu Ala Val Glu
 510 515 520

cac gtg aag ttt ctg ata agg gag gcg tgg aag gag atg aac acg gtc 1636
 His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Glu Met Asn Thr Val
 525 530 535

aca aca gcc agc gat tgt ccg ttt acg gat gat ttg gtt gcg gcc gca 1684
 Thr Thr Ala Ser Asp Cys Pro Phe Thr Asp Asp Leu Val Ala Ala Ala
 540 545 550

gct aat ctt gca agg gcg gct cag ttt ata tat ctc gac ggg gat ggg 1732
 Ala Asn Leu Ala Arg Ala Ala Gln Phe Ile Tyr Leu Asp Gly Asp Gly
 555 560 565

cat ggc gtg caa cac tca gaa ata cat caa cag atg gga ggc ctg cta 1780
 His Gly Val Gln His Ser Glu Ile His Gln Gln Met Gly Gly Leu Leu
 570 575 580 585

ttc cag cct tat gtctgaataa atcgaaaatc caacctacta tgtatccctc 1832
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atcctcaaaa aaaaaaaaaa 1912

<210> 48
 <211> 589
 <212> PRT
 <213> Artificial Sequence

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Pro Ala Ala Arg Leu Arg Ala Ser Ser Ser Leu Gln Gln Glu Lys Pro
 35 40 45

His Gln Ile Arg Arg Ser Gly Asp Tyr Gln Pro Ser Leu Trp Asp Phe
 50 55 60

Asn Tyr Ile Gln Ser Ile Asn Thr Pro Tyr Lys Glu Gln Arg His Phe
 65 70 75 80

Asn Arg Gln Ala Glu Leu Ile Met Gln Val Arg Met Leu Leu Lys Val
 85 90 95
 Lys Met Glu Ala Ile Gln Gln Leu Glu Leu Ile Asp Asp Leu Gln Tyr
 100 105 110
 Leu Gly Leu Ser Tyr Phe Phe Gln Asp Glu Ile Lys Gln Ile Leu Ser
 115 120 125
 Ser Ile His Asn Glu Pro Arg Tyr Phe His Asn Asn Asp Leu Tyr Phe
 130 135 140
 Thr Ala Leu Gly Phe Arg Ile Leu Arg Gln His Gly Phe Asn Val Ser
 145 150 155 160
 Glu Asp Val Phe Asp Cys Phe Lys Ile Glu Lys Cys Ser Asp Phe Asn
 165 170 175
 Ala Asn Leu Ala Gln Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala
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 Ser Phe Leu Leu Arg Glu Gly Glu Asp Thr Leu Glu Leu Ala Arg Arg
 195 200 205
 Phe Ser Thr Arg Ser Leu Arg Glu Lys Phe Asp Glu Gly Gly Asp Glu
 210 215 220
 Ile Asp Glu Asp Leu Ser Ser Trp Ile Arg His Ser Leu Asp Leu Pro
 225 230 235 240
 Leu His Trp Arg Val Gln Gly Leu Glu Ala Arg Trp Phe Leu Asp Ala
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 Tyr Ala Arg Arg Pro Asp Met Asn Pro Leu Ile Phe Lys Leu Ala Lys
 260 265 270
 Leu Asn Phe Asn Ile Val Gln Ala Thr Tyr Gln Glu Glu Leu Lys Asp
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 305 310 315 320
 Glu Pro His Gln Tyr Ser Tyr Gln Arg Lys Met Ala Ala Val Ile Ile
 325 330 335
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 Glu Glu Leu Glu Leu Leu Thr Asp Met Ile Arg Arg Trp Asp Asn Lys
 355 360 365
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 Tyr Asn Phe Val Ser Glu Arg Ala Tyr Asp Ile Leu Lys Asp Gln His
 385 390 395 400

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Leu	Glu	Glu	Tyr	Leu	Asn	Asn	Ala	Lys	Ile	Ser	Ile	Ser	Ala	Pro	Thr
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Ile	Ile	Ser	Gln	Leu	Tyr	Phe	Thr	Leu	Ala	Asn	Ser	Ile	Asp	Glu	Thr
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Glu	Arg	Gly	Asp	Val	Pro	Lys	Ala	Ile	Gln	Cys	Tyr	Met	Asn	Asp	Thr
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Gln	Phe	Ile	Tyr	Leu	Asp	Gly	Asp	Gly	His	Gly	Val	Gln	His	Ser	Glu
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<210> 49
<211> 1912
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:
computer-generated nucleic acid sequence

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<220>
<221> CDS
<222> (26)..(1792)
<223> computer-generated nucleic acid sequence encoding
      (+)-sabinene synthase

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<400> 49
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Met Pro Leu Asn Ser Leu His Asn Phe Glu Arg Lys Pro Ser Lys Ala
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Gln Pro Ser Leu Trp Asp Phe Asn Tyr Ile Gln Ser Leu Asn Thr Pro	
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Val Arg Met Leu Leu Lys Val Lys Met Glu Ala Ile Gln Gln Leu Glu	
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Leu Ile Asp Asp Leu Gln Tyr Leu Gly Leu Ser Tyr Phe Phe Gln Asp	
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 510 515 520

cac gtg aag ttt ctg ata agg gag gcg tgg aag gag atg aac acg gtc 1636
 His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Glu Met Asn Thr Val
 525 530 535

aca aca gcc agc gat tgt ccg ttt acg gat gat ttg gtt gcg gcc gca 1684
 Thr Thr Ala Ser Asp Cys Pro Phe Thr Asp Asp Leu Val Ala Ala Ala
 540 545 550

gct aat ctt gca agg gcg gct cag ttt ata tat ctc gac ggg gat ggg 1732
 Ala Asn Leu Ala Arg Ala Ala Gln Phe Ile Tyr Leu Asp Gly Asp Gly
 555 560 565

cat ggc gtg caa cac tca gaa ata cat caa cag atg gga ggc ctg cta 1780
 His Gly Val Gln His Ser Glu Ile His Gln Gln Met Gly Gly Leu Leu
 570 575 580 585

ttc cag cct tat gtctgaataa atcgaaaatc caacctacta tgtatccctc 1832
 Phe Gln Pro Tyr

gataatatat tcttgggggtt aacatgttta attaaagttc taattdaaag agctgaatcg 1892
 atcctcaaaa aaaaaaaaaa 1912

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 <211> 589
 <212> PRT
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 35 40 45
 His Gln Ile Arg Arg Ser Gly Asp Tyr Gln Pro Ser Leu Trp Asp Phe
 50 55 60
 Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Lys Glu Gln Arg His Phe
 65 70 75 80
 Asn Arg Gln Ala Glu Val Ile Met Gln Val Arg Met Leu Leu Lys Val
 85 90 95
 Lys Met Glu Ala Ile Gln Gln Leu Glu Leu Ile Asp Asp Leu Gln Tyr
 100 105 110
 Leu Gly Leu Ser Tyr Phe Phe Gln Asp Glu Ile Lys Gln Ile Leu Ser
 115 120 125
 Ser Ile His Asn Glu Pro Arg Tyr Phe His Asn Asn Asp Leu Tyr Phe

130	135	140
Thr Ala Leu Gly Phe Arg Ile Leu Arg Gln His Gly Phe Asn Val Ser 145 150 155 160		
Glu Asp Val Phe Asp Cys Phe Lys Ile Glu Lys Cys Ser Asp Phe Asn 165 170 175		
Ala Asn Leu Ala Gln Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala 180 185 190		
Ser Phe Leu Leu Arg Glu Gly Glu Asp Thr Leu Glu Leu Ala Arg Arg 195 200 205		
Phe Ser Thr Arg Ser Leu Arg Glu Lys Phe Asp Glu Gly Gly Asp Glu 210 215 220		
Ile Asp Glu Asp Leu Ser Ser Trp Ile Arg His Ser Leu Asp Leu Pro 225 230 235 240		
Leu His Trp Arg Val Gln Gly Leu Glu Ala Arg Trp Phe Leu Asp Ala 245 250 255		
Tyr Ala Arg Arg Pro Asp Met Asn Pro Leu Ile Phe Lys Leu Ala Lys 260 265 270		
Leu Asn Phe Asn Ile Val Gln Ala Thr Tyr Gln Glu Glu Leu Lys Asp 275 280 285		
Ile Ser Arg Trp Trp Asn Ser Ser Cys Leu Ala Glu Lys Leu Pro Phe 290 295 300		
Val Arg Asp Arg Ile Val Glu Cys Phe Phe Trp Ala Ile Ala Ala Phe 305 310 315 320		
Glu Pro His Gln Tyr Ser Tyr Gln Arg Lys Met Ala Ala Val Ile Ile 325 330 335		
Thr Phe Ile Thr Ile Ile Asp Asp Val Tyr Asp Val Tyr Gly Thr Ile 340 345 350		
Glu Glu Leu Glu Leu Leu Thr Asp Met Ile Arg Arg Trp Asp Asn Lys 355 360 365		
Ser Ile Ser Gln Leu Pro Tyr Tyr Met Gln Val Cys Tyr Leu Ala Leu 370 375 380		
Tyr Asn Phe Val Ser Glu Arg Ala Tyr Asp Ile Leu Lys Asp Gln His 385 390 395 400		
Phe Asn Ser Ile Pro Tyr Leu Gln Arg Ser Trp Val Ser Leu Val Glu 405 410 415		
Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr Tyr Asn Gly Tyr Lys Pro Ser 420 425 430		
Leu Glu Glu Tyr Leu Asn Asn Ala Lys Ile Ser Ile Ser Ala Pro Thr 435 440 445		
Ile Ile Ser Gln Leu Tyr Phe Thr Leu Ala Asn Ser Ile Asp Glu Thr		

450											455											460
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Thr	Ile	Leu	Arg	Leu 485	Ala	Asp	Asp	Leu	Gly 490	Thr	Ser	Gln	His	Glu 495	Leu							
Glu	Arg	Gly	Asp 500	Val	Pro	Lys	Ala	Ile 505	Gln	Cys	Tyr	Met	Asn 510	Asp	Thr							
Asn	Ala	Ser 515	Glu	Arg	Glu	Ala	Val 520	Glu	His	Val	Lys	Phe 525	Leu	Ile	Arg							
Glu 530	Ala	Trp	Lys	Glu	Met	Asn 535	Thr	Val	Thr	Thr	Ala 540	Ser	Asp	Cys	Pro							
Phe 545	Thr	Asp	Asp	Leu	Val 550	Ala	Ala	Ala	Ala	Asn 555	Leu	Ala	Arg	Ala	Ala 560							
Gln	Phe	Ile	Tyr	Leu 565	Asp	Gly	Asp	Gly	His 570	Gly	Val	Gln	His	Ser 575	Glu							
Ile	His	Gln	Gln	Met	Gly	Gly	Leu	Leu	Phe	Gln	Pro	Tyr										
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<210> 51

<211> 1912

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
computer-generated nucleic acid sequence

<220>

<221> CDS

<222> (26) .. (1792)

<223> computer-generated nucleic acid sequence encoding (+)-sabinene synthase

<400> 51

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1 5

atg cca ctg aat tcc ctc cac aac ttt gag agg aaa cct tca aaa gca 100
Met Pro Leu Asn Ser Leu His Asn Phe Glu Arg Lys Pro Ser Lys Ala
10 15 20 25

tgg tct acc tct tgc act gca ccc gca gct cgc ctg cgg gca tct tcc 148
Trp Ser Thr Ser Cys Thr Ala Pro Ala Ala Arg Leu Arg Ala Ser Ser

30 35 40

tcc tta caa caa gaa aaa cct cac caa atc cga cgc tct ggg gat tac 196
Ser Leu Gln Gln Glu Lys Pro His Gln Ile Arg Arg Ser Gly Asp Tyr
45 50 55

caa ccc tct ctt tgg gat ttc aat tac ata cag tct ctc aac act ccg 244

Gln	Pro	Ser	Leu	Trp	Asp	Phe	Asn	Tyr	Ile	Gln	Ser	Leu	Asn	Thr	Pro	
	60						65					70				
tat	aag	gag	cag	aga	cac	ttt	aat	agg	caa	gca	gag	ttg	att	atg	caa	292
Tyr	Lys	Glu	Gln	Arg	His	Phe	Asn	Arg	Gln	Ala	Glu	Leu	Ile	Met	Gln	
	75					80				85						
gtg	agg	atg	ttg	ctc	aag	gta	aag	atg	gag	gca	ctt	caa	cag	ttg	gag	340
Val	Arg	Met	Leu	Leu	Lys	Val	Lys	Met	Glu	Ala	Leu	Gln	Gln	Leu	Glu	
	90				95				100					105		
ttg	att	gat	gac	ttg	caa	tac	ctg	gga	ctg	tct	tat	ttc	ttt	caa	gat	388
Leu	Ile	Asp	Asp	Leu	Gln	Tyr	Leu	Gly	Leu	Ser	Tyr	Phe	Phe	Gln	Asp	
				110				115						120		
gag	att	aaa	caa	atc	tta	agt	tct	ata	cac	aat	gag	ccc	aga	tat	ttc	436
Glu	Ile	Lys	Gln	Ile	Leu	Ser	Ser	Ile	His	Asn	Glu	Pro	Arg	Tyr	Phe	
			125					130					135			
cac	aat	aat	gat	ttg	tat	ttc	aca	gct	ctt	gga	ttc	aga	atc	ctc	aga	484
His	Asn	Asn	Asp	Leu	Tyr	Phe	Thr	Ala	Leu	Gly	Phe	Arg	Ile	Leu	Arg	
			140				145					150				
caa	cat	ggt	ttt	aat	gtt	tcc	gaa	gat	gta	ttt	gat	tgt	ttc	aaa	att	532
Gln	His	Gly	Phe	Asn	Val	Ser	Glu	Asp	Val	Phe	Asp	Cys	Phe	Lys	Ile	
	155					160					165					
gag	aag	tgc	agt	gat	ttc	aat	gca	aac	ctt	gct	caa	gat	acg	aag	gga	580
Glu	Lys	Cys	Ser	Asp	Phe	Asn	Ala	Asn	Leu	Ala	Gln	Asp	Thr	Lys	Gly	
	170				175				180					185		
atg	tta	caa	ctt	tat	gaa	gca	tct	ttc	ctt	ttg	aga	gaa	ggt	gaa	gat	628
Met	Leu	Gln	Leu	Tyr	Glu	Ala	Ser	Phe	Leu	Leu	Arg	Glu	Gly	Glu	Asp	
				190				195						200		
aca	ttg	gag	cta	gca	aga	cga	ttt	tcc	acc	aga	tct	cta	cga	gaa	aaa	676
Thr	Leu	Glu	Leu	Ala	Arg	Arg	Phe	Ser	Thr	Arg	Ser	Leu	Arg	Glu	Lys	
			205					210					215			
ttt	gat	gaa	ggt	ggt	gat	gaa	att	gat	gaa	gat	cta	tca	tcg	tggt	att	724
Phe	Asp	Glu	Gly	Gly	Asp	Glu	Ile	Asp	Glu	Asp	Leu	Ser	Ser	Trp	Ile	
		220				225						230				
cgc	cat	tcc	ttg	gat	ctt	cct	ctt	cat	tgg	agg	gtc	caa	gga	tta	gag	772
Arg	His	Ser	Leu	Asp	Leu	Pro	Leu	His	Trp	Arg	Val	Gln	Gly	Leu	Glu	
	235					240					245					
gca	aga	tgg	ttc	tta	gat	gct	tat	gcg	agg	agg	ccg	gac	atg	aat	cca	820
Ala	Arg	Trp	Phe	Leu	Asp	Ala	Tyr	Ala	Arg	Arg	Pro	Asp	Met	Asn	Pro	
	250				255				260					265		
ctt	att	ttc	aaa	ctc	gcc	aaa	ctc	aac	ttc	aat	att	gtt	cag	gca	aca	868
Leu	Ile	Phe	Lys	Leu	Ala	Lys	Leu	Asn	Phe	Asn	Ile	Val	Gln	Ala	Thr	
				270				275					280			
tat	caa	gaa	gaa	ctg	aaa	gat	atc	tca	agg	tgg	tgg	aat	agt	tcg	tgc	916
Tyr	Gln	Glu	Glu	Leu	Lys	Asp	Ile	Ser	Arg	Trp	Trp	Asn	Ser	Ser	Cys	
			285					290					295			
ctt	gct	gag	aaa	ctc	cca	ttt	gtg	aga	gat	agg	att	gtg	gaa	tgc	ttc	964

Leu Ala Glu Lys Leu Pro Phe Val Arg Asp Arg Ile Val Glu Cys Phe
 300 305 310
 ttt tgg gcc atc gcg gct ttt gag cct cac caa tat agt tat cag aga 1012
 Phe Trp Ala Ile Ala Ala Phe Glu Pro His Gln Tyr Ser Tyr Gln Arg
 315 320 325
 aaa atg gcc gcc gtt att att act ttc ata aca att atc gat gat gtt 1060
 Lys Met Ala Ala Val Ile Ile Thr Phe Ile Thr Ile Ile Asp Asp Val
 330 335 340 345
 tat gat gtg tat gga aca ata gaa gaa cta gaa cta tta aca gat atg 1108
 Tyr Asp Val Tyr Gly Thr Ile Glu Glu Leu Glu Leu Leu Thr Asp Met
 350 355 360
 att cgc aga tgg gat aat aaa tca ata agc caa ctt cca tat tat atg 1156
 Ile Arg Arg Trp Asp Asn Lys Ser Ile Ser Gln Leu Pro Tyr Tyr Met
 365 370 375
 caa gtg tgc tat ttg gca cta tac aac ttc gtt tct gag cgg gct tac 1204
 Gln Val Cys Tyr Leu Ala Leu Tyr Asn Phe Val Ser Glu Arg Ala Tyr
 380 385 390
 gat att cta aaa gat caa cat ttc aac agc atc cca tat tta cag aga 1252
 Asp Ile Leu Lys Asp Gln His Phe Asn Ser Ile Pro Tyr Leu Gln Arg
 395 400 405
 tcg tgg gta agt ttg gtt gaa gga tat ctt aag gag gca tac tgg tac 1300
 Ser Trp Val Ser Leu Val Glu Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr
 410 415 420 425
 tac aat ggc tat aaa cca agc ttg gaa gaa tat ctc aac aac gcc aag 1348
 Tyr Asn Gly Tyr Lys Pro Ser Leu Glu Glu Tyr Leu Asn Asn Ala Lys
 430 435 440
 att tca ata tcg gct cct aca atc ata tcc cag ctt tat ttt aca tta 1396
 Ile Ser Ile Ser Ala Pro Thr Ile Ile Ser Gln Leu Tyr Phe Thr Leu
 445 450 455
 gca aac tcg att gat gaa aca gct atc gag agc ttg tac caa tat cat 1444
 Ala Asn Ser Ile Asp Glu Thr Ala Ile Glu Ser Leu Tyr Gln Tyr His
 460 465 470
 aac ata ctt tac cta tca gga acc ata tta agg ctt gct gac gat ctt 1492
 Asn Ile Leu Tyr Leu Ser Gly Thr Ile Leu Arg Leu Ala Asp Asp Leu
 475 480 485
 ggg aca tca caa cat gag ctg gag aga gga gac gta ccg aaa gca atc 1540
 Gly Thr Ser Gln His Glu Leu Glu Arg Gly Asp Val Pro Lys Ala Ile
 490 495 500 505
 cag tgc tac atg aat gac aca aat gct tcg gag aga gag gcg gtg gaa 1588
 Gln Cys Tyr Met Asn Asp Thr Asn Ala Ser Glu Arg Glu Ala Val Glu
 510 515 520
 cac gtg aag ttt ctg ata agg gag gcg tgg aag gag atg aac acg gtc 1636
 His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Glu Met Asn Thr Val
 525 530 535
 aca aca gcc agc gat tgt ccg ttt acg gat gat ttg gtt gcg gcc gca 1684

Thr Thr Ala Ser Asp Cys Pro Phe Thr Asp Asp Leu Val Ala Ala Ala
 540 545 550
 gct aat ctt gca agg gcg gct cag ttt ata tat ctc gac ggg gat ggg 1732
 Ala Asn Leu Ala Arg Ala Ala Gln Phe Ile Tyr Leu Asp Gly Asp Gly
 555 560 565
 cat ggc gtg caa cac tca gaa ata cat caa cag atg gga ggc ctg cta 1780
 His Gly Val Gln His Ser Glu Ile His Gln Gln Met Gly Gly Leu Leu
 570 575 580 585
 ttc cag cct tat gtctgaataa atcgaaaatc caacctacta tgtatccctc 1832
 Phe Gln Pro Tyr
 gataatatat tcttgggggtt aacatgttta attaaagttc taattdaaag agctgaatcg 1892
 atcctcaaaa aaaaaaaaaa 1912

 <210> 52
 <211> 589
 <212> PRT
 <213> Artificial Sequence

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 Pro Ala Ala Arg Leu Arg Ala Ser Ser Leu Gln Gln Glu Lys Pro
 35 40 45
 His Gln Ile Arg Arg Ser Gly Asp Tyr Gln Pro Ser Leu Trp Asp Phe
 50 55 60
 Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Lys Glu Gln Arg His Phe
 65 70 75 80
 Asn Arg Gln Ala Glu Leu Ile Met Gln Val Arg Met Leu Leu Lys Val
 85 90 95
 Lys Met Glu Ala Leu Gln Gln Leu Glu Leu Ile Asp Asp Leu Gln Tyr
 100 105 110
 Leu Gly Leu Ser Tyr Phe Phe Gln Asp Glu Ile Lys Gln Ile Leu Ser
 115 120 125
 Ser Ile His Asn Glu Pro Arg Tyr Phe His Asn Asn Asp Leu Tyr Phe
 130 135 140
 Thr Ala Leu Gly Phe Arg Ile Leu Arg Gln His Gly Phe Asn Val Ser
 145 150 155 160
 Glu Asp Val Phe Asp Cys Phe Lys Ile Glu Lys Cys Ser Asp Phe Asn
 165 170 175
 Ala Asn Leu Ala Gln Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala
 180 185 190

Ser Phe Leu Leu Arg Glu Gly Glu Asp Thr Leu Glu Leu Ala Arg Arg
 195 200 205
 Phe Ser Thr Arg Ser Leu Arg Glu Lys Phe Asp Glu Gly Gly Asp Glu
 210 215 220
 Ile Asp Glu Asp Leu Ser Ser Trp Ile Arg His Ser Leu Asp Leu Pro
 225 230 235 240
 Leu His Trp Arg Val Gln Gly Leu Glu Ala Arg Trp Phe Leu Asp Ala
 245 250 255
 Tyr Ala Arg Arg Pro Asp Met Asn Pro Leu Ile Phe Lys Leu Ala Lys
 260 265 270
 Leu Asn Phe Asn Ile Val Gln Ala Thr Tyr Gln Glu Glu Leu Lys Asp
 275 280 285
 Ile Ser Arg Trp Trp Asn Ser Ser Cys Leu Ala Glu Lys Leu Pro Phe
 290 295 300
 Val Arg Asp Arg Ile Val Glu Cys Phe Phe Trp Ala Ile Ala Ala Phe
 305 310 315 320
 Glu Pro His Gln Tyr Ser Tyr Gln Arg Lys Met Ala Ala Val Ile Ile
 325 330 335
 Thr Phe Ile Thr Ile Ile Asp Asp Val Tyr Asp Val Tyr Gly Thr Ile
 340 345 350
 Glu Glu Leu Glu Leu Leu Thr Asp Met Ile Arg Arg Trp Asp Asn Lys
 355 360 365
 Ser Ile Ser Gln Leu Pro Tyr Tyr Met Gln Val Cys Tyr Leu Ala Leu
 370 375 380
 Tyr Asn Phe Val Ser Glu Arg Ala Tyr Asp Ile Leu Lys Asp Gln His
 385 390 395 400
 Phe Asn Ser Ile Pro Tyr Leu Gln Arg Ser Trp Val Ser Leu Val Glu
 405 410 415
 Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr Tyr Asn Gly Tyr Lys Pro Ser
 420 425 430
 Leu Glu Glu Tyr Leu Asn Asn Ala Lys Ile Ser Ile Ser Ala Pro Thr
 435 440 445
 Ile Ile Ser Gln Leu Tyr Phe Thr Leu Ala Asn Ser Ile Asp Glu Thr
 450 455 460
 Ala Ile Glu Ser Leu Tyr Gln Tyr His Asn Ile Leu Tyr Leu Ser Gly
 465 470 475 480
 Thr Ile Leu Arg Leu Ala Asp Asp Leu Gly Thr Ser Gln His Glu Leu
 485 490 495
 Glu Arg Gly Asp Val Pro Lys Ala Ile Gln Cys Tyr Met Asn Asp Thr
 500 505 510

Asn Ala Ser Glu Arg Glu Ala Val Glu His Val Lys Phe Leu Ile Arg
 515 520 525

Glu Ala Trp Lys Glu Met Asn Thr Val Thr Thr Ala Ser Asp Cys Pro
 530 535 540

Phe Thr Asp Asp Leu Val Ala Ala Ala Asn Leu Ala Arg Ala Ala
 545 550 555 560

Gln Phe Ile Tyr Leu Asp Gly Asp Gly His Gly Val Gln His Ser Glu
 565 570 575

Ile His Gln Gln Met Gly Gly Leu Leu Phe Gln Pro Tyr
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<210> 53

<211> 1912

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 computer-generated nucleic acid sequence

<220>

<221> CDS

<222> (26)..(1792)

<223> computer-generated nucleic acid sequence encoding
 (+)-sabinene synthase

<400> 53

agcaatatta caactaacaa taaaa atg tct tcc att agc ata aac ata gct 52
 Met Ser Ser Ile Ser Ile Asn Ile Ala
 1 5

atg cca ctg aat tcc ctc cac aac ttt gag agg aaa cct tca aaa gca 100
 Met Pro Leu Asn Ser Leu His Asn Phe Glu Arg Lys Pro Ser Lys Ala
 10 15 20 25

tgg tct acc tct tgc act gca ccc gca gct cgc ctc cgg gca tct tcc 148
 Trp Ser Thr Ser Cys Thr Ala Pro Ala Ala Arg Leu Arg Ala Ser Ser
 30 35 40

tcc tta caa caa gaa aaa cct cac caa atc cga cgc tct ggg gat tac 196
 Ser Leu Gln Gln Glu Lys Pro His Gln Ile Arg Arg Ser Gly Asp Tyr
 45 50 55

caa ccc tct ctt tgg gat ttc aat tac ata cag tct ctc aac act ccg 244
 Gln Pro Ser Leu Trp Asp Phe Asn Tyr Ile Gln Ser Leu Asn Thr Pro
 60 65 70

tat aag gag cag aga cac ttt aat agg caa gca gag ttg att atg caa 292
 Tyr Lys Glu Gln Arg His Phe Asn Arg Gln Ala Glu Leu Ile Met Gln
 75 80 85

gtg agg atg ttg ctc aag gta aag atg gag gca att caa cag gtg gag 340
 Val Arg Met Leu Leu Lys Val Lys Met Glu Ala Ile Gln Gln Val Glu
 90 95 100 105

ttg att gat gac ttg caa tac ctg gga ctg tct tat ttc ttt caa gat Leu Ile Asp Asp Leu Gln Tyr Leu Gly Leu Ser Tyr Phe Phe Gln Asp	388
110 115 120	
gag att aaa caa atc tta agt tct ata cac aat gag ccc aga tat ttc Glu Ile Lys Gln Ile Leu Ser Ser Ile His Asn Glu Pro Arg Tyr Phe	436
125 130 135	
cac aat aat gat ttg tat ttc aca gct ctt gga ttc aga atc ctc aga His Asn Asn Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Ile Leu Arg	484
140 145 150	
caa cat ggt ttt aat gtt tcc gaa gat gta ttt gat tgt ttc aaa att Gln His Gly Phe Asn Val Ser Glu Asp Val Phe Asp Cys Phe Lys Ile	532
155 160 165	
gag aag tgc agt gat ttc aat gca aac ctt gct caa gat acg aag gga Glu Lys Cys Ser Asp Phe Asn Ala Asn Leu Ala Gln Asp Thr Lys Gly	580
170 175 180 185	
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190 195 200	
aca ttg gag cta gca aga cga ttt tcc acc aga tct cta cga gaa aaa Thr Leu Glu Leu Ala Arg Arg Phe Ser Thr Arg Ser Leu Arg Glu Lys	676
205 210 215	
ttt. gat gaa ggt ggt gat gaa att gat gaa gat cta tca tgc tgg att Phe Asp Glu Gly Gly Asp Glu Ile Asp Glu Asp Leu Ser Ser Trp Ile	724
220 225 230	
cgc cat tcc ttg gat ctt cct ctt cat tgg agg gtc caa gga tta gag Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Val Gln Gly Leu Glu	772
235 240 245	
gca aga tgg ttc tta gat gct tat gcg agg agg ccg gac atg aat cca Ala Arg Trp Phe Leu Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn Pro	820
250 255 260 265	
ctt att ttc aaa ctc gcc aaa ctc aac ttc aat att gtt cag gca aca Leu Ile Phe Lys Leu Ala Lys Leu Asn Phe Asn Ile Val Gln Ala Thr	868
270 275 280	
tat caa gaa gaa ctg aaa gat atc tca agg tgg tgg aat agt tgc tgc Tyr Gln Glu Glu Leu Lys Asp Ile Ser Arg Trp Trp Asn Ser Ser Cys	916
285 290 295	
ctt gct gag aaa ctc cca ttt gtg aga gat agg att gtg gaa tgc ttc Leu Ala Glu Lys Leu Pro Phe Val Arg Asp Arg Ile Val Glu Cys Phe	964
300 305 310	
ttt tgg gcc atc gcg gct ttt gag cct cac caa tat agt tat cag aga Phe Trp Ala Ile Ala Ala Phe Glu Pro His Gln Tyr Ser Tyr Gln Arg	1012
315 320 325	
aaa atg gcc gcc gtt att att act ttc ata aca att atc gat gat gtt Lys Met Ala Ala Val Ile Ile Thr Phe Ile Thr Ile Ile Asp Asp Val	1060
330 335 340 345	

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caa gtg tgc tat ttg gca cta tac aac ttc gtt tct gag cgg gct tac Gln Val Cys Tyr Leu Ala Leu Tyr Asn Phe Val Ser Glu Arg Ala Tyr 380 385 390	1204
gat att cta aaa gat caa cat ttc aac agc atc cca tat tta cag aga Asp Ile Leu Lys Asp Gln His Phe Asn Ser Ile Pro Tyr Leu Gln Arg 395 400 405	1252
tcg tgg gta agt ttg gtt gaa gga tat ctt aag gag gca tac tgg tac Ser Trp Val Ser Leu Val Glu Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr 410 415 420 425	1300
tac aat ggc tat aaa cca agc ttg gaa gaa tat ctc aac aac gcc aag Tyr Asn Gly Tyr Lys Pro Ser Leu Glu Glu Tyr Leu Asn Asn Ala Lys 430 435 440	1348
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gca aac tcg att gat gaa aca gct atc gag agc ttg tac caa tat cat Ala Asn Ser Ile Asp Glu Thr Ala Ile Glu Ser Leu Tyr Gln Tyr His 460 465 470	1444
aac ata ctt tac cta tca gga acc ata tta agg ctt gct gac gat ctt Asn Ile Leu Tyr Leu Ser Gly Thr Ile Leu Arg Leu Ala Asp Asp Leu 475 480 485	1492
ggg aca tca caa cat gag ctg gag aga gga gac gta ccg aaa gca atc Gly Thr Ser Gln His Glu Leu Glu Arg Gly Asp Val Pro Lys Ala Ile 490 495 500 505	1540
cag tgc tac atg aat gac aca aat gct tcg gag aga gag gcg gtg gaa Gln Cys Tyr Met Asn Asp Thr Asn Ala Ser Glu Arg Glu Ala Val Glu 510 515 520	1588
cac gtg aag ttt ctg ata agg gag gcg tgg aag gag atg aac acg gtc His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Glu Met Asn Thr Val 525 530 535	1636
aca aca gcc agc gat tgt ccg ttt acg gat gat ttg gtt gcg gcc gca Thr Thr Ala Ser Asp Cys Pro Phe Thr Asp Asp Leu Val Ala Ala Ala 540 545 550	1684
gct aat ctt gca agg gcg gct cag ttt ata tat ctc gac ggg gat ggg Ala Asn Leu Ala Arg Ala Ala Gln Phe Ile Tyr Leu Asp Gly Asp Gly 555 560 565	1732
cat ggc gtg caa cac tca gaa ata cat caa cag atg gga ggc ctg cta His Gly Val Gln His Ser Glu Ile His Gln Gln Met Gly Gly Leu Leu 570 575 580 585	1780

ttc cag cct tat gtctgaataa atcgaaaatc caacctacta tgtatccctc 1832
Phe Gln Pro Tyr

gataatatat tcttgggggtt aacatgttta attaaagttc taattdaaag agctgaatcg 1892

atcctcaaaa aaaaaaaaaa 1912

<210> 54

<211> 589

<212> PRT

<213> Artificial Sequence

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1 5 10 15
Asn Phe Glu Arg Lys Pro Ser Lys Ala Trp Ser Thr Ser Cys Thr Ala
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35 40 45
His Gln Ile Arg Arg Ser Gly Asp Tyr Gln Pro Ser Leu Trp Asp Phe
50 55 60
Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Lys Glu Gln Arg His Phe
65 70 75 80
Asn Arg Gln Ala Glu Leu Ile Met Gln Val Arg Met Leu Leu Lys Val
85 90 95
Lys Met Glu Ala Ile Gln Gln Val Glu Leu Ile Asp Asp Leu Gln Tyr
100 105 110
Leu Gly Leu Ser Tyr Phe Phe Gln Asp Glu Ile Lys Gln Ile Leu Ser
115 120 125
Ser Ile His Asn Glu Pro Arg Tyr Phe His Asn Asn Asp Leu Tyr Phe
130 135 140
Thr Ala Leu Gly Phe Arg Ile Leu Arg Gln His Gly Phe Asn Val Ser
145 150 155 160
Glu Asp Val Phe Asp Cys Phe Lys Ile Glu Lys Cys Ser Asp Phe Asn
165 170 175
Ala Asn Leu Ala Gln Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala
180 185 190
Ser Phe Leu Leu Arg Glu Gly Glu Asp Thr Leu Glu Leu Ala Arg Arg
195 200 205
Phe Ser Thr Arg Ser Leu Arg Glu Lys Phe Asp Glu Gly Gly Asp Glu
210 215 220
Ile Asp Glu Asp Leu Ser Ser Trp Ile Arg His Ser Leu Asp Leu Pro
225 230 235 240

Leu His Trp Arg Val Gln Gly Leu Glu Ala Arg Trp Phe Leu Asp Ala
 245 250 255
 Tyr Ala Arg Arg Pro Asp Met Asn Pro Leu Ile Phe Lys Leu Ala Lys
 260 265 270
 Leu Asn Phe Asn Ile Val Gln Ala Thr Tyr Gln Glu Glu Leu Lys Asp
 275 280 285
 Ile Ser Arg Trp Trp Asn Ser Ser Cys Leu Ala Glu Lys Leu Pro Phe
 290 295 300
 Val Arg Asp Arg Ile Val Glu Cys Phe Phe Trp Ala Ile Ala Ala Phe
 305 310 315 320
 Glu Pro His Gln Tyr Ser Tyr Gln Arg Lys Met Ala Ala Val Ile Ile
 325 330 335
 Thr Phe Ile Thr Ile Ile Asp Asp Val Tyr Asp Val Tyr Gly Thr Ile
 340 345 350
 Glu Glu Leu Glu Leu Leu Thr Asp Met Ile Arg Arg Trp Asp Asn Lys
 355 360 365
 Ser Ile Ser Gln Leu Pro Tyr Tyr Met Gln Val Cys Tyr Leu Ala Leu
 370 375 380
 Tyr Asn Phe Val Ser Glu Arg Ala Tyr Asp Ile Leu Lys Asp Gln His
 385 390 395 400
 Phe Asn Ser Ile Pro Tyr Leu Gln Arg Ser Trp Val Ser Leu Val Glu
 405 410 415
 Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr Tyr Asn Gly Tyr Lys Pro Ser
 420 425 430
 Leu Glu Glu Tyr Leu Asn Asn Ala Lys Ile Ser Ile Ser Ala Pro Thr
 435 440 445
 Ile Ile Ser Gln Leu Tyr Phe Thr Leu Ala Asn Ser Ile Asp Glu Thr
 450 455 460
 Ala Ile Glu Ser Leu Tyr Gln Tyr His Asn Ile Leu Tyr Leu Ser Gly
 465 470 475 480
 Thr Ile Leu Arg Leu Ala Asp Asp Leu Gly Thr Ser Gln His Glu Leu
 485 490 495
 Glu Arg Gly Asp Val Pro Lys Ala Ile Gln Cys Tyr Met Asn Asp Thr
 500 505 510
 Asn Ala Ser Glu Arg Glu Ala Val Glu His Val Lys Phe Leu Ile Arg
 515 520 525
 Glu Ala Trp Lys Glu Met Asn Thr Val Thr Thr Ala Ser Asp Cys Pro
 530 535 540
 Phe Thr Asp Asp Leu Val Ala Ala Ala Ala Asn Leu Ala Arg Ala Ala
 545 550 555 560

Gln Phe Ile Tyr Leu Asp Gly Asp Gly His Gly Val Gln His Ser Glu
 565 570 575

Ile His Gln Gln Met Gly Gly Leu Leu Phe Gln Pro Tyr
 580 585

<210> 55

<211> 1912

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 computer-generated nucleic acid sequence

<220>

<221> CDS

<222> (26)..(1792)

<223> (+)-sabinene synthase encoded by computer
 generated nucleic acid sequence

<400> 55

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                        1 5

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Met Pro Leu Asn Ser Leu His Asn Phe Glu Arg Lys Pro Ser Lys Ala
10 15 20 25

tgg tct acc tct tgc act gca ccc gca gct cgc ctc cgg gca tct tcc 148
Trp Ser Thr Ser Cys Thr Ala Pro Ala Ala Arg Leu Arg Ala Ser Ser
30 35 40

tcc tta caa caa gaa aaa cct cac caa atc cga cgc tct ggg gat tac 196
Ser Leu Gln Gln Glu Lys Pro His Gln Ile Arg Arg Ser Gly Asp Tyr
45 50 55

caa ccc tct ctt tgg gat ttc aat tac ata cag tct ctc aac act ccg 244
Gln Pro Ser Leu Trp Asp Phe Asn Tyr Ile Gln Ser Leu Asn Thr Pro
60 65 70

tat aag gag cag aga cac ttt aat agg caa gca gag ttg att atg caa 292
Tyr Lys Glu Gln Arg His Phe Asn Arg Gln Ala Glu Leu Ile Met Gln
75 80 85

gtg agg atg ttg ctc aag gta aag atg gag gca att caa cag ttg gag 340
Val Arg Met Leu Leu Lys Val Lys Met Glu Ala Ile Gln Gln Leu Glu
90 95 100 105

gtg att gat gac ttg caa tac ctg gga ctg tct tat ttc ttt caa gat 388
Val Ile Asp Asp Leu Gln Tyr Leu Gly Leu Ser Tyr Phe Phe Gln Asp
110 115 120

gag att aaa caa atc tta agt tct ata cac aat gag ccc aga tat ttc 436
Glu Ile Lys Gln Ile Leu Ser Ser Ile His Asn Glu Pro Arg Tyr Phe
125 130 135

cac aat aat gat ttg tat ttc aca gct ctt gga ttc aga atc ctc aga 484

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His Asn Asn Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Ile Leu Arg
 140 145 150
 caa cat ggt ttt aat gtt tcc gaa gat gta ttt gat tgt ttc aaa att 532
 Gln His Gly Phe Asn Val Ser Glu Asp Val Phe Asp Cys Phe Lys Ile
 155 160 165
 gag aag tgc agt gat ttc aat gca aac ctt gct caa gat acg aag gga 580
 Glu Lys Cys Ser Asp Phe Asn Ala Asn Leu Ala Gln Asp Thr Lys Gly
 170 175 180 185
 atg tta caa ctt tat gaa gca tct ttc ctt ttg aga gaa ggt gaa gat 628
 Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Glu Gly Glu Asp
 190 195 200
 aca ttg gag cta gca aga cga ttt tcc acc aga tct cta cga gaa aaa 676
 Thr Leu Glu Leu Ala Arg Arg Phe Ser Thr Arg Ser Leu Arg Glu Lys
 205 210 215
 ttt gat gaa ggt ggt gat gaa att gat gaa gat cta tca tcg tgg att 724
 Phe Asp Glu Gly Gly Asp Glu Ile Asp Glu Asp Leu Ser Ser Trp Ile
 220 225 230
 cgc cat tcc ttg gat ctt cct ctt cat tgg agg gtc caa gga tta gag 772
 Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Val Gln Gly Leu Glu
 235 240 245
 gca aga tgg ttc tta gat gct tat gcg agg agg ccg gac atg aat cca 820
 Ala Arg Trp Phe Leu Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn Pro
 250 255 260 265
 ctt att ttc aaa ctc gcc aaa ctc aac ttc aat att gtt cag gca aca 868
 Leu Ile Phe Lys Leu Ala Lys Leu Asn Phe Asn Ile Val Gln Ala Thr
 270 275 280
 tat caa gaa gaa ctg aaa gat atc tca agg tgg tgg aat agt tcg tgc 916
 Tyr Gln Glu Glu Leu Lys Asp Ile Ser Arg Trp Trp Asn Ser Ser Cys
 285 290 295
 ctt gct gag aaa ctc cca ttt gtg aga gat agg att gtg gaa tgc ttc 964
 Leu Ala Glu Lys Leu Pro Phe Val Arg Asp Arg Ile Val Glu Cys Phe
 300 305 310
 ttt tgg gcc atc gcg gct ttt gag cct cac caa tat agt tat cag aga 1012
 Phe Trp Ala Ile Ala Ala Phe Glu Pro His Gln Tyr Ser Tyr Gln Arg
 315 320 325
 aaa atg gcc gcc gtt att att act ttc ata aca att atc gat gat gtt 1060
 Lys Met Ala Ala Val Ile Ile Thr Phe Ile Thr Ile Ile Asp Asp Val
 330 335 340 345
 tat gat gtg tat gga aca ata gaa gaa cta gaa cta tta aca gat atg 1108
 Tyr Asp Val Tyr Gly Thr Ile Glu Glu Leu Glu Leu Leu Thr Asp Met
 350 355 360
 att cgc aga tgg gat aat aaa tca ata agc caa ctt cca tat tat atg 1156
 Ile Arg Arg Trp Asp Asn Lys Ser Ile Ser Gln Leu Pro Tyr Tyr Met
 365 370 375
 caa gtg tgc tat ttg gca cta tac aac ttc gtt tct gag cgg gct tac 1204

Gln Val Cys Tyr Leu Ala Leu Tyr Asn Phe Val Ser Glu Arg Ala Tyr
 380 385 390
 gat att cta aaa gat caa cat ttc aac agc atc cca tat tta cag aga 1252
 Asp Ile Leu Lys Asp Gln His Phe Asn Ser Ile Pro Tyr Leu Gln Arg
 395 400 405
 tcg tgg gta agt ttg gtt gaa gga tat ctt aag gag gca tac tgg tac 1300
 Ser Trp Val Ser Leu Val Glu Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr
 410 415 420 425
 tac aat ggc tat aaa cca agc ttg gaa gaa tat ctc aac aac gcc aag 1348
 Tyr Asn Gly Tyr Lys Pro Ser Leu Glu Glu Tyr Leu Asn Asn Ala Lys
 430 435 440
 att tca ata tcg gct cct aca atc ata tcc cag ctt tat ttt aca tta 1396
 Ile Ser Ile Ser Ala Pro Thr Ile Ile Ser Gln Leu Tyr Phe Thr Leu
 445 450 455
 gca aac tcg att gat gaa aca gct atc gag agc ttg tac caa tat cat 1444
 Ala Asn Ser Ile Asp Glu Thr Ala Ile Glu Ser Leu Tyr Gln Tyr His
 460 465 470
 aac ata ctt tac cta tca gga acc ata tta agg ctt gct gac gat ctt 1492
 Asn Ile Leu Tyr Leu Ser Gly Thr Ile Leu Arg Leu Ala Asp Asp Leu
 475 480 485
 ggg aca tca caa cat gag ctg gag aga gga gac gta ccg aaa gca atc 1540
 Gly Thr Ser Gln His Glu Leu Glu Arg Gly Asp Val Pro Lys Ala Ile
 490 495 500 505
 cag tgc tac atg aat gac aca aat gct tcg gag aga gag gcg gtg gaa 1588
 Gln Cys Tyr Met Asn Asp Thr Asn Ala Ser Glu Arg Glu Ala Val Glu
 510 515 520
 cac gtg aag ttt ctg ata agg gag gcg tgg aag gag atg aac acg gtc 1636
 His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Glu Met Asn Thr Val
 525 530 535
 aca aca gcc agc gat tgt ccg ttt acg gat gat ttg gtt gcg gcc gca 1684
 Thr Thr Ala Ser Asp Cys Pro Phe Thr Asp Asp Leu Val Ala Ala Ala
 540 545 550
 gct aat ctt gca agg gcg gct cag ttt ata tat ctc gac ggg gat ggg 1732
 Ala Asn Leu Ala Arg Ala Ala Gln Phe Ile Tyr Leu Asp Gly Asp Gly
 555 560 565
 cat ggc gtg caa cac tca gaa ata cat caa cag atg gga ggc ctg cta 1780
 His Gly Val Gln His Ser Glu Ile His Gln Gln Met Gly Gly Leu Leu
 570 575 580 585
 ttc cag cct tat gtctgaataa atcgaaaatc caacctacta tgtatccctc 1832
 Phe Gln Pro Tyr
 gataatatat tcttgggggtt aacatgttta attaaagttc taattdaaag agctgaatcg 1892
 atcctcaaaa aaaaaaaaaa 1912

<210> 56

<211> 589

<212> PRT

<213> Artificial Sequence

<400> 56

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Met Ser Ser Ile Ser Ile Asn Ile Ala Met Pro Leu Asn Ser Leu His
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Asn Phe Glu Arg Lys Pro Ser Lys Ala Trp Ser Thr Ser Cys Thr Ala
           20           25           30
Pro Ala Ala Arg Leu Arg Ala Ser Ser Ser Leu Gln Gln Glu Lys Pro
           35           40           45
His Gln Ile Arg Arg Ser Gly Asp Tyr Gln Pro Ser Leu Trp Asp Phe
           50           55           60
Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Lys Glu Gln Arg His Phe
           65           70           75           80
Asn Arg Gln Ala Glu Leu Ile Met Gln Val Arg Met Leu Leu Lys Val
           85           90           95
Lys Met Glu Ala Ile Gln Gln Leu Glu Val Ile Asp Asp Leu Gln Tyr
           100          105          110
Leu Gly Leu Ser Tyr Phe Phe Gln Asp Glu Ile Lys Gln Ile Leu Ser
           115          120          125
Ser Ile His Asn Glu Pro Arg Tyr Phe His Asn Asn Asp Leu Tyr Phe
           130          135          140
Thr Ala Leu Gly Phe Arg Ile Leu Arg Gln His Gly Phe Asn Val Ser
           145          150          155          160
Glu Asp Val Phe Asp Cys Phe Lys Ile Glu Lys Cys Ser Asp Phe Asn
           165          170          175
Ala Asn Leu Ala Gln Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala
           180          185          190
Ser Phe Leu Leu Arg Glu Gly Glu Asp Thr Leu Glu Leu Ala Arg Arg
           195          200          205
Phe Ser Thr Arg Ser Leu Arg Glu Lys Phe Asp Glu Gly Gly Asp Glu
           210          215          220
Ile Asp Glu Asp Leu Ser Ser Trp Ile Arg His Ser Leu Asp Leu Pro
           225          230          235          240
Leu His Trp Arg Val Gln Gly Leu Glu Ala Arg Trp Phe Leu Asp Ala
           245          250          255
Tyr Ala Arg Arg Pro Asp Met Asn Pro Leu Ile Phe Lys Leu Ala Lys
           260          265          270
Leu Asn Phe Asn Ile Val Gln Ala Thr Tyr Gln Glu Glu Leu Lys Asp
           275          280          285
Ile Ser Arg Trp Trp Asn Ser Ser Cys Leu Ala Glu Lys Leu Pro Phe

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290	295	300
Val Arg Asp Arg Ile Val Glu Cys Phe Phe Trp Ala Ile Ala Ala Phe 305 310 315 320		
Glu Pro His Gln Tyr Ser Tyr Gln Arg Lys Met Ala Ala Val Ile Ile 325 330 335		
Thr Phe Ile Thr Ile Ile Asp Asp Val Tyr Asp Val Tyr Gly Thr Ile 340 345 350		
Glu Glu Leu Glu Leu Leu Thr Asp Met Ile Arg Arg Trp Asp Asn Lys 355 360 365		
Ser Ile Ser Gln Leu Pro Tyr Tyr Met Gln Val Cys Tyr Leu Ala Leu 370 375 380		
Tyr Asn Phe Val Ser Glu Arg Ala Tyr Asp Ile Leu Lys Asp Gln His 385 390 395 400		
Phe Asn Ser Ile Pro Tyr Leu Gln Arg Ser Trp Val Ser Leu Val Glu 405 410 415		
Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr Tyr Asn Gly Tyr Lys Pro Ser 420 425 430		
Leu Glu Glu Tyr Leu Asn Asn Ala Lys Ile Ser Ile Ser Ala Pro Thr 435 440 445		
Ile Ile Ser Gln Leu Tyr Phe Thr Leu Ala Asn Ser Ile Asp Glu Thr 450 455 460		
Ala Ile Glu Ser Leu Tyr Gln Tyr His Asn Ile Leu Tyr Leu Ser Gly 465 470 475 480		
Thr Ile Leu Arg Leu Ala Asp Asp Leu Gly Thr Ser Gln His Glu Leu 485 490 495		
Glu Arg Gly Asp Val Pro Lys Ala Ile Gln Cys Tyr Met Asn Asp Thr 500 505 510		
Asn Ala Ser Glu Arg Glu Ala Val Glu His Val Lys Phe Leu Ile Arg 515 520 525		
Glu Ala Trp Lys Glu Met Asn Thr Val Thr Thr Ala Ser Asp Cys Pro 530 535 540		
Phe Thr Asp Asp Leu Val Ala Ala Ala Ala Asn Leu Ala Arg Ala Ala 545 550 555 560		
Gln Phe Ile Tyr Leu Asp Gly Asp Gly His Gly Val Gln His Ser Glu 565 570 575		
Ile His Gln Gln Met Gly Gly Leu Leu Phe Gln Pro Tyr 580 585		

<210> 57
 <211> 1912
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
computer-generated nucleic acid sequence

<220>

<221> CDS

<222> (26)..(1792)

<223> computer-generated nucleic acid sequence encoding
(+)-sabinene synthase

<400> 57

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                        1                               5

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Met Pro Leu Asn Ser Leu His Asn Phe Glu Arg Lys Pro Ser Lys Ala
10                      15                      20          25

tgg tct acc tct tgc act gca ccc gca gct cgc ctc cgg gca tct tcc 148
Trp Ser Thr Ser Cys Thr Ala Pro Ala Ala Arg Leu Arg Ala Ser Ser
                      30                      35          40

tcc tta caa caa gaa aaa cct cac caa atc cga cgc tct ggg gat tac 196
Ser Leu Gln Gln Glu Lys Pro His Gln Ile Arg Arg Ser Gly Asp Tyr
                      45                      50          55

caa ccc tct ctt tgg gat ttc aat tac ata cag tct ctc aac act ccg 244
Gln Pro Ser Leu Trp Asp Phe Asn Tyr Ile Gln Ser Leu Asn Thr Pro
                      60                      65          70

tat aag gag cag aga cac ttt aat agg caa gca gag ttg att atg caa 292
Tyr Lys Glu Gln Arg His Phe Asn Arg Gln Ala Glu Leu Ile Met Gln
75                      80                      85

gtg agg atg ttg ctc aag gta aag atg gag gca att caa cag ttg gag 340
Val Arg Met Leu Leu Lys Val Lys Met Glu Ala Ile Gln Gln Leu Glu
90                      95                      100         105

ttg att gat gac gtg caa tac ctg gga ctg tct tat ttc ttt caa gat 388
Leu Ile Asp Asp Val Gln Tyr Leu Gly Leu Ser Tyr Phe Phe Gln Asp
110                      115                      120

gag att aaa caa atc tta agt tct ata cac aat gag ccc aga tat ttc 436
Glu Ile Lys Gln Ile Leu Ser Ser Ile His Asn Glu Pro Arg Tyr Phe
125                      130                      135

cac aat aat gat ttg tat ttc aca gct ctt gga ttc aga atc ctc aga 484
His Asn Asn Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Ile Leu Arg
140                      145                      150

caa cat ggt ttt aat gtt tcc gaa gat gta ttt gat tgt ttc aaa att 532
Gln His Gly Phe Asn Val Ser Glu Asp Val Phe Asp Cys Phe Lys Ile
155                      160                      165

gag aag tgc agt gat ttc aat gca aac ctt gct caa gat acg aag gga 580
Glu Lys Cys Ser Asp Phe Asn Ala Asn Leu Ala Gln Asp Thr Lys Gly
170                      175                      180         185

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atg tta caa ctt tat gaa gca tct ttc ctt ttg aga gaa ggt gaa gat Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Glu Gly Glu Asp 190 195 200	628
aca ttg gag cta gca aga cga ttt tcc acc aga tct cta cga gaa aaa Thr Leu Glu Leu Ala Arg Arg Phe Ser Thr Arg Ser Leu Arg Glu Lys 205 210 215	676
ttt gat gaa ggt ggt gat gaa att gat gaa gat cta tca tcg tgg att Phe Asp Glu Gly Gly Asp Glu Ile Asp Glu Asp Leu Ser Ser Trp Ile 220 225 230	724
cgc cat tcc ttg gat ctt cct ctt cat tgg agg gtc caa gga tta gag Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Val Gln Gly Leu Glu 235 240 245	772
gca aga tgg ttc tta gat gct tat gcg agg agg ccg gac atg aat cca Ala Arg Trp Phe Leu Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn Pro 250 255 260 265	820
ctt att ttc aaa ctc gcc aaa ctc aac ttc aat att gtt cag gca aca Leu Ile Phe Lys Leu Ala Lys Leu Asn Phe Asn Ile Val Gln Ala Thr 270 275 280	868
tat caa gaa gaa ctg aaa gat atc tca agg tgg tgg aat agt tcg tgc Tyr Gln Glu Glu Leu Lys Asp Ile Ser Arg Trp Trp Asn Ser Ser Cys 285 290 295	916
ctt gct gag aaa ctc cca ttt gtg aga gat agg att gtg gaa tgc ttc Leu Ala Glu Lys Leu Pro Phe Val Arg Asp Arg Ile Val Glu Cys Phe 300 305 310	964
ttt tgg gcc atc gcg gct ttt gag cct cac caa tat agt tat cag aga Phe Trp Ala Ile Ala Ala Phe Glu Pro His Gln Tyr Ser Tyr Gln Arg 315 320 325	1012
aaa atg gcc gcc gtt att att act ttc ata aca att atc gat gat gtt Lys Met Ala Ala Val Ile Ile Thr Phe Ile Thr Ile Ile Asp Asp Val 330 335 340 345	1060
tat gat gtg tat gga aca ata gaa gaa cta gaa cta tta aca gat atg Tyr Asp Val Tyr Gly Thr Ile Glu Glu Leu Glu Leu Leu Thr Asp Met 350 355 360	1108
att cgc aga tgg gat aat aaa tca ata agc caa ctt cca tat tat atg Ile Arg Arg Trp Asp Asn Lys Ser Ile Ser Gln Leu Pro Tyr Tyr Met 365 370 375	1156
caa gtg tgc tat ttg gca cta tac aac ttc gtt tct gag cgg gct tac Gln Val Cys Tyr Leu Ala Leu Tyr Asn Phe Val Ser Glu Arg Ala Tyr 380 385 390	1204
gat att cta aaa gat caa cat ttc aac agc atc cca tat tta cag aga Asp Ile Leu Lys Asp Gln His Phe Asn Ser Ile Pro Tyr Leu Gln Arg 395 400 405	1252
tcg tgg gta agt ttg gtt gaa gga tat ctt aag gag gca tac tgg tac Ser Trp Val Ser Leu Val Glu Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr 410 415 420 425	1300

tac aat ggc tat aaa cca agc ttg gaa gaa tat ctc aac aac gcc aag 1348
 Tyr Asn Gly Tyr Lys Pro Ser Leu Glu Glu Tyr Leu Asn Asn Ala Lys
 430 435 440

att tca ata tcg gct cct aca atc ata tcc cag ctt tat ttt aca tta 1396
 Ile Ser Ile Ser Ala Pro Thr Ile Ile Ser Gln Leu Tyr Phe Thr Leu
 445 450 455

gca aac tcg att gat gaa aca gct atc gag agc ttg tac caa tat cat 1444
 Ala Asn Ser Ile Asp Glu Thr Ala Ile Glu Ser Leu Tyr Gln Tyr His
 460 465 470

aac ata ctt tac cta tca gga acc ata tta agg ctt gct gac gat ctt 1492
 Asn Ile Leu Tyr Leu Ser Gly Thr Ile Leu Arg Leu Ala Asp Asp Leu
 475 480 485

ggg aca tca caa cat gag ctg gag aga gga gac gta ccg aaa gca atc 1540
 Gly Thr Ser Gln His Glu Leu Glu Arg Gly Asp Val Pro Lys Ala Ile
 490 495 500 505

cag tgc tac atg aat gac aca aat gct tcg gag aga gag gcg gtg gaa 1588
 Gln Cys Tyr Met Asn Asp Thr Asn Ala Ser Glu Arg Glu Ala Val Glu
 510 515 520

cac gtg aag ttt ctg ata agg gag gcg tgg aag gag atg aac acg gtc 1636
 His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Glu Met Asn Thr Val
 525 530 535

aca aca gcc agc gat tgt ccg ttt acg gat gat ttg gtt gcg gcc gca 1684
 Thr Thr Ala Ser Asp Cys Pro Phe Thr Asp Asp Leu Val Ala Ala Ala
 540 545 550

gct aat ctt gca agg gcg gct cag ttt ata tat ctc gac ggg gat ggg 1732
 Ala Asn Leu Ala Arg Ala Ala Gln Phe Ile Tyr Leu Asp Gly Asp Gly
 555 560 565

cat ggc gtg caa cac tca gaa ata cat caa cag atg gga ggc ctg cta 1780
 His Gly Val Gln His Ser Glu Ile His Gln Gln Met Gly Gly Leu Leu
 570 575 580 585

ttc cag cct tat gtctgaataa atcgaaaatc caacctacta tgtatccctc 1832
 Phe Gln Pro Tyr

gataatatat tcttgggggtt aacatgttta attaaagtcc taattdaaag agctgaatcg 1892

atcctcaaaa aaaaaaaaaa 1912

<210> 58
 <211> 589
 <212> PRT
 <213> Artificial Sequence

<400> 58
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 Asn Phe Glu Arg Lys Pro Ser Lys Ala Trp Ser Thr Ser Cys Thr Ala
 20 25 30

Pro Ala Ala Arg Leu Arg Ala Ser Ser Ser Leu Gln Gln Glu Lys Pro
 35 40 45
 His Gln Ile Arg Arg Ser Gly Asp Tyr Gln Pro Ser Leu Trp Asp Phe
 50 55 60
 Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Lys Glu Gln Arg His Phe
 65 70 75 80
 Asn Arg Gln Ala Glu Leu Ile Met Gln Val Arg Met Leu Leu Lys Val
 85 90 95
 Lys Met Glu Ala Ile Gln Gln Leu Glu Leu Ile Asp Asp Val Gln Tyr
 100 105 110
 Leu Gly Leu Ser Tyr Phe Phe Gln Asp Glu Ile Lys Gln Ile Leu Ser
 115 120 125
 Ser Ile His Asn Glu Pro Arg Tyr Phe His Asn Asn Asp Leu Tyr Phe
 130 135 140
 Thr Ala Leu Gly Phe Arg Ile Leu Arg Gln His Gly Phe Asn Val Ser
 145 150 155 160
 Glu Asp Val Phe Asp Cys Phe Lys Ile Glu Lys Cys Ser Asp Phe Asn
 165 170 175
 Ala Asn Leu Ala Gln Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala
 180 185 190
 Ser Phe Leu Leu Arg Glu Gly Glu Asp Thr Leu Glu Leu Ala Arg Arg
 195 200 205
 Phe Ser Thr Arg Ser Leu Arg Glu Lys Phe Asp Glu Gly Gly Asp Glu
 210 215 220
 Ile Asp Glu Asp Leu Ser Ser Trp Ile Arg His Ser Leu Asp Leu Pro
 225 230 235 240
 Leu His Trp Arg Val Gln Gly Leu Glu Ala Arg Trp Phe Leu Asp Ala
 245 250 255
 Tyr Ala Arg Arg Pro Asp Met Asn Pro Leu Ile Phe Lys Leu Ala Lys
 260 265 270
 Leu Asn Phe Asn Ile Val Gln Ala Thr Tyr Gln Glu Glu Leu Lys Asp
 275 280 285
 Ile Ser Arg Trp Trp Asn Ser Ser Cys Leu Ala Glu Lys Leu Pro Phe
 290 295 300
 Val Arg Asp Arg Ile Val Glu Cys Phe Phe Trp Ala Ile Ala Ala Phe
 305 310 315 320
 Glu Pro His Gln Tyr Ser Tyr Gln Arg Lys Met Ala Ala Val Ile Ile
 325 330 335
 Thr Phe Ile Thr Ile Ile Asp Asp Val Tyr Asp Val Tyr Gly Thr Ile
 340 345 350

Glu Glu Leu Glu Leu Leu Thr Asp Met Ile Arg Arg Trp Asp Asn Lys
 355 360 365
 Ser Ile Ser Gln Leu Pro Tyr Tyr Met Gln Val Cys Tyr Leu Ala Leu
 370 375 380
 Tyr Asn Phe Val Ser Glu Arg Ala Tyr Asp Ile Leu Lys Asp Gln His
 385 390 395 400
 Phe Asn Ser Ile Pro Tyr Leu Gln Arg Ser Trp Val Ser Leu Val Glu
 405 410 415
 Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr Tyr Asn Gly Tyr Lys Pro Ser
 420 425 430
 Leu Glu Glu Tyr Leu Asn Asn Ala Lys Ile Ser Ile Ser Ala Pro Thr
 435 440 445
 Ile Ile Ser Gln Leu Tyr Phe Thr Leu Ala Asn Ser Ile Asp Glu Thr
 450 455 460
 Ala Ile Glu Ser Leu Tyr Gln Tyr His Asn Ile Leu Tyr Leu Ser Gly
 465 470 475 480
 Thr Ile Leu Arg Leu Ala Asp Asp Leu Gly Thr Ser Gln His Glu Leu
 485 490 495
 Glu Arg Gly Asp Val Pro Lys Ala Ile Gln Cys Tyr Met Asn Asp Thr
 500 505 510
 Asn Ala Ser Glu Arg Glu Ala Val Glu His Val Lys Phe Leu Ile Arg
 515 520 525
 Glu Ala Trp Lys Glu Met Asn Thr Val Thr Thr Ala Ser Asp Cys Pro
 530 535 540
 Phe Thr Asp Asp Leu Val Ala Ala Ala Ala Asn Leu Ala Arg Ala Ala
 545 550 555 560
 Gln Phe Ile Tyr Leu Asp Gly Asp Gly His Gly Val Gln His Ser Glu
 565 570 575
 Ile His Gln Gln Met Gly Gly Leu Leu Phe Gln Pro Tyr
 580 585

<210> 59

<211> 1912

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 computer-generated nucleic acid sequence

<220>

<221> CDS

<222> (26) .. (1792)

<223> computer-generated nucleic acid sequence encoding

(+) -sabinene synthase

<400> 59

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Met Pro Leu Asn Ser Leu His Asn Phe Glu Arg Lys Pro Ser Lys Ala
10 15 20 25

tgg tct acc tct tgc act gca ccc gca gct cgc ctc cgg gca tct tcc 148
Trp Ser Thr Ser Cys Thr Ala Pro Ala Ala Arg Leu Arg Ala Ser Ser
30 35 40

tcc tta caa caa gaa aaa cct cac caa atc cga cgc tct ggg gat tac 196
Ser Leu Gln Gln Glu Lys Pro His Gln Ile Arg Arg Ser Gly Asp Tyr
45 50 55

caa ccc tct ctt tgg gat ttc aat tac ata cag tct ctc aac act ccg 244
Gln Pro Ser Leu Trp Asp Phe Asn Tyr Ile Gln Ser Leu Asn Thr Pro
60 65 70

tat aag gag cag aga cac ttt aat agg caa gca gag ttg att atg caa 292
Tyr Lys Glu Gln Arg His Phe Asn Arg Gln Ala Glu Leu Ile Met Gln
75 80 85

gtg agg atg ttg ctc aag gta aag atg gag gca att caa cag ttg gag 340
Val Arg Met Leu Leu Lys Val Lys Met Glu Ala Ile Gln Gln Leu Glu
90 95 100 105

ttg att gat gac ttg caa tac gtg gga ctg tct tat ttc ttt caa gat 388
Leu Ile Asp Asp Leu Gln Tyr Val Gly Leu Ser Tyr Phe Phe Gln Asp
110 115 120

gag att aaa caa atc tta agt tct ata cac aat gag ccc aga tat ttc 436
Glu Ile Lys Gln Ile Leu Ser Ser Ile His Asn Glu Pro Arg Tyr Phe
125 130 135

cac aat aat gat ttg tat ttc aca gct ctt gga ttc aga atc ctc aga 484
His Asn Asn Asp Leu Tyr Phe Thr Ala Leu Gly Phe Arg Ile Leu Arg
140 145 150

caa cat ggt ttt aat gtt tcc gaa gat gta ttt gat tgt ttc aaa att 532
Gln His Gly Phe Asn Val Ser Glu Asp Val Phe Asp Cys Phe Lys Ile
155 160 165

gag aag tgc agt gat ttc aat gca aac ctt gct caa gat acg aag gga 580
Glu Lys Cys Ser Asp Phe Asn Ala Asn Leu Ala Gln Asp Thr Lys Gly
170 175 180 185

atg tta caa ctt tat gaa gca tct ttc ctt ttg aga gaa ggt gaa gat 628
Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg Glu Gly Glu Asp
190 195 200

aca ttg gag cta gca aga cga ttt tcc acc aga tct cta cga gaa aaa 676
Thr Leu Glu Leu Ala Arg Arg Phe Ser Thr Arg Ser Leu Arg Glu Lys
205 210 215

ttt gat gaa ggt ggt gat gaa att gat gaa gat cta tca tcg tgg att 724

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Phe Asp Glu Gly Gly Asp Glu Ile Asp Glu Asp Leu Ser Ser Trp Ile 220 225 230	
cgc cat tcc ttg gat ctt cct ctt cat tgg agg gtc caa gga tta gag Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Val Gln Gly Leu Glu 235 240 245	772
gca aga tgg ttc tta gat gct tat gcg agg agg ccg gac atg aat cca Ala Arg Trp Phe Leu Asp Ala Tyr Ala Arg Arg Pro Asp Met Asn Pro 250 255 260 265	820
ctt att ttc aaa ctc gcc aaa ctc aac ttc aat att gtt cag gca aca Leu Ile Phe Lys Leu Ala Lys Leu Asn Phe Asn Ile Val Gln Ala Thr 270 275 280	868
tat caa gaa gaa ctg aaa gat atc tca agg tgg tgg aat agt tcg tgc Tyr Gln Glu Glu Leu Lys Asp Ile Ser Arg Trp Trp Asn Ser Ser Cys 285 290 295	916
ctt gct gag aaa ctc cca ttt gtg aga gat agg att gtg gaa tgc ttc Leu Ala Glu Lys Leu Pro Phe Val Arg Asp Arg Ile Val Glu Cys Phe 300 305 310	964
ttt tgg gcc atc gcg gct ttt gag cct cac caa tat agt tat cag aga Phe Trp Ala Ile Ala Ala Phe Glu Pro His Gln Tyr Ser Tyr Gln Arg 315 320 325	1012
aaa atg gcc gcc gtt att att act ttc ata aca att atc gat gat gtt Lys Met Ala Ala Val Ile Ile Thr Phe Ile Thr Ile Ile Asp Asp Val 330 335 340 345	1060
tat gat gtg tat gga aca ata gaa gaa cta gaa cta tta aca gat atg Tyr Asp Val Tyr Gly Thr Ile Glu Glu Leu Glu Leu Leu Thr Asp Met 350 355 360	1108
att cgc aga tgg gat aat aaa tca ata agc caa ctt cca tat tat atg Ile Arg Arg Trp Asp Asn Lys Ser Ile Ser Gln Leu Pro Tyr Tyr Met 365 370 375	1156
caa gtg tgc tat ttg gca cta tac aac ttc gtt tct gag cgg gct tac Gln Val Cys Tyr Leu Ala Leu Tyr Asn Phe Val Ser Glu Arg Ala Tyr 380 385 390	1204
gat att cta aaa gat caa cat ttc aac agc atc cca tat tta cag aga Asp Ile Leu Lys Asp Gln His Phe Asn Ser Ile Pro Tyr Leu Gln Arg 395 400 405	1252
tcg tgg gta agt ttg gtt gaa gga tat ctt aag gag gca tac tgg tac Ser Trp Val Ser Leu Val Glu Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr 410 415 420 425	1300
tac aat ggc tat aaa cca agc ttg gaa gaa tat ctc aac aac gcc aag Tyr Asn Gly Tyr Lys Pro Ser Leu Glu Glu Tyr Leu Asn Asn Ala Lys 430 435 440	1348
att tca ata tcg gct cct aca atc ata tcc cag ctt tat ttt aca tta Ile Ser Ile Ser Ala Pro Thr Ile Ile Ser Gln Leu Tyr Phe Thr Leu 445 450 455	1396
gca aac tcg att gat gaa aca gct atc gag agc ttg tac caa tat cat	1444

Ala Asn Ser Ile Asp Glu Thr Ala Ile Glu Ser Leu Tyr Gln Tyr His
 460 465 470

aac ata ctt tac cta tca gga acc ata tta agg ctt gct gac gat ctt 1492
 Asn Ile Leu Tyr Leu Ser Gly Thr Ile Leu Arg Leu Ala Asp Asp Leu
 475 480 485

ggg aca tca caa cat gag ctg gag aga gga gac gta ccg aaa gca atc 1540
 Gly Thr Ser Gln His Glu Leu Glu Arg Gly Asp Val Pro Lys Ala Ile
 490 495 500 505

cag tgc tac atg aat gac aca aat gct tcg gag aga gag gcg gtg gaa 1588
 Gln Cys Tyr Met Asn Asp Thr Asn Ala Ser Glu Arg Glu Ala Val Glu
 510 515 520

cac gtg aag ttt ctg ata agg gag gcg tgg aag gag atg aac acg gtc 1636
 His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Glu Met Asn Thr Val
 525 530 535

aca aca gcc agc gat tgt ccg ttt acg gat gat ttg gtt gcg gcc gca 1684
 Thr Thr Ala Ser Asp Cys Pro Phe Thr Asp Asp Leu Val Ala Ala Ala
 540 545 550

gct aat ctt gca agg gcg gct cag ttt ata tat ctg gac ggg gat ggg 1732
 Ala Asn Leu Ala Arg Ala Ala Gln Phe Ile Tyr Leu Asp Gly Asp Gly
 555 560 565

cat ggc gtg caa cac tca gaa ata cat caa cag atg gga ggc ctg cta 1780
 His Gly Val Gln His Ser Glu Ile His Gln Gln Met Gly Gly Leu Leu
 570 575 580 585

ttc cag cct tat gtctgaataa atcgaaaatc caacctacta tgtatccctc 1832
 Phe Gln Pro Tyr

gataatatat tcttggggtt aacatgttta attaaagttc taattdaaag agctgaatcg 1892

atcctcaaaa aaaaaaaaaa 1912

<210> 60

<211> 589

<212> PRT

<213> Artificial Sequence

<400> 60

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Asn Phe Glu Arg Lys Pro Ser Lys Ala Trp Ser Thr Ser Cys Thr Ala
 20 25 30

Pro Ala Ala Arg Leu Arg Ala Ser Ser Ser Leu Gln Gln Glu Lys Pro
 35 40 45

His Gln Ile Arg Arg Ser Gly Asp Tyr Gln Pro Ser Leu Trp Asp Phe
 50 55 60

Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Lys Glu Gln Arg His Phe
 65 70 75 80

Asn Arg Gln Ala Glu Leu Ile Met Gln Val Arg Met Leu Leu Lys Val
 85 90 95
 Lys Met Glu Ala Ile Gln Gln Leu Glu Leu Ile Asp Asp Leu Gln Tyr
 100 105 110
 Val Gly Leu Ser Tyr Phe Phe Gln Asp Glu Ile Lys Gln Ile Leu Ser
 115 120 125
 Ser Ile His Asn Glu Pro Arg Tyr Phe His Asn Asn Asp Leu Tyr Phe
 130 135 140
 Thr Ala Leu Gly Phe Arg Ile Leu Arg Gln His Gly Phe Asn Val Ser
 145 150 155 160
 Glu Asp Val Phe Asp Cys Phe Lys Ile Glu Lys Cys Ser Asp Phe Asn
 165 170 175
 Ala Asn Leu Ala Gln Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala
 180 185 190
 Ser Phe Leu Leu Arg Glu Gly Glu Asp Thr Leu Glu Leu Ala Arg Arg
 195 200 205
 Phe Ser Thr Arg Ser Leu Arg Glu Lys Phe Asp Glu Gly Gly Asp Glu
 210 215 220
 Ile Asp Glu Asp Leu Ser Ser Trp Ile Arg His Ser Leu Asp Leu Pro
 225 230 235 240
 Leu His Trp Arg Val Gln Gly Leu Glu Ala Arg Trp Phe Leu Asp Ala
 245 250 255
 Tyr Ala Arg Arg Pro Asp Met Asn Pro Leu Ile Phe Lys Leu Ala Lys
 260 265 270
 Leu Asn Phe Asn Ile Val Gln Ala Thr Tyr Gln Glu Glu Leu Lys Asp
 275 280 285
 Ile Ser Arg Trp Trp Asn Ser Ser Cys Leu Ala Glu Lys Leu Pro Phe
 290 295 300
 Val Arg Asp Arg Ile Val Glu Cys Phe Phe Trp Ala Ile Ala Ala Phe
 305 310 315 320
 Glu Pro His Gln Tyr Ser Tyr Gln Arg Lys Met Ala Ala Val Ile Ile
 325 330 335
 Thr Phe Ile Thr Ile Ile Asp Asp Val Tyr Asp Val Tyr Gly Thr Ile
 340 345 350
 Glu Glu Leu Glu Leu Leu Thr Asp Met Ile Arg Arg Trp Asp Asn Lys
 355 360 365
 Ser Ile Ser Gln Leu Pro Tyr Tyr Met Gln Val Cys Tyr Leu Ala Leu
 370 375 380
 Tyr Asn Phe Val Ser Glu Arg Ala Tyr Asp Ile Leu Lys Asp Gln His
 385 390 395 400

Phe Asn Ser Ile Pro Tyr Leu Gln Arg Ser Trp Val Ser Leu Val Glu
 405 410 415
 Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr Tyr Asn Gly Tyr Lys Pro Ser
 420 425 430
 Leu Glu Glu Tyr Leu Asn Asn Ala Lys Ile Ser Ile Ser Ala Pro Thr
 435 440 445
 Ile Ile Ser Gln Leu Tyr Phe Thr Leu Ala Asn Ser Ile Asp Glu Thr
 450 455 460
 Ala Ile Glu Ser Leu Tyr Gln Tyr His Asn Ile Leu Tyr Leu Ser Gly
 465 470 475 480
 Thr Ile Leu Arg Leu Ala Asp Asp Leu Gly Thr Ser Gln His Glu Leu
 485 490 495
 Glu Arg Gly Asp Val Pro Lys Ala Ile Gln Cys Tyr Met Asn Asp Thr
 500 505 510
 Asn Ala Ser Glu Arg Glu Ala Val Glu His Val Lys Phe Leu Ile Arg
 515 520 525
 Glu Ala Trp Lys Glu Met Asn Thr Val Thr Thr Ala Ser Asp Cys Pro
 530 535 540
 Phe Thr Asp Asp Leu Val Ala Ala Ala Asn Leu Ala Arg Ala Ala
 545 550 555 560
 Gln Phe Ile Tyr Leu Asp Gly Asp Gly His Gly Val Gln His Ser Glu
 565 570 575
 Ile His Gln Gln Met Gly Gly Leu Leu Phe Gln Pro Tyr
 580 585

<210> 61

<211> 590

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

computer-generated (+)-sabinene synthase protein

<220>

<221> VARIANT

<222> (1)..(590)

<223> computer-generated (+)-sabinene synthase protein
sequence variant

<400> 61

Met Ser Ser Ile Ser Ile Asn Ile Ala Met Pro Leu Asn Ser Leu His
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Asn Phe Glu Arg Lys Pro Ser Lys Ala Trp Ser Thr Ser Cys Thr Ala
 20 25 30

Pro Ala Ala Arg Leu Arg Ala Ser Ser Ser Leu Gln Gln Glu Lys Pro

35					40					45					
His	Gln	Ile	Arg	Arg	Ser	Gly	Asp	Tyr	Gln	Pro	Ser	Ile	Trp	Asp	Phe
50						55					60				
Asn	Tyr	Ile	Gln	Ser	Leu	Asn	Thr	Pro	Tyr	Lys	Glu	Gln	Arg	His	Phe
65					70					75					80
Asn	Arg	Gln	Ala	Glu	Leu	Ile	Met	Gln	Val	Arg	Met	Leu	Leu	Lys	Val
				85					90					95	
Lys	Met	Glu	Ala	Ile	Gln	Gln	Leu	Glu	Leu	Ile	Asp	Asp	Leu	Gln	Tyr
			100					105					110		
Leu	Gly	Leu	Ser	Tyr	Phe	Phe	Gln	Asp	Glu	Ile	Lys	Gln	Ile	Leu	Ser
		115					120					125			
Ser	Ile	His	Asn	Glu	Pro	Arg	Tyr	Phe	His	Asn	Asn	Asp	Leu	Tyr	Phe
130					135					140					
Thr	Ala	Leu	Gly	Phe	Arg	Ile	Leu	Arg	Gln	His	Gly	Phe	Asn	Val	Ser
145				150						155					160
Glu	Asp	Val	Phe	Asp	Cys	Phe	Lys	Ile	Glu	Lys	Cys	Ser	Asp	Phe	Asn
				165					170					175	
Ala	Asn	Leu	Ala	Gln	Asp	Thr	Lys	Gly	Met	Leu	Gln	Leu	Tyr	Glu	Ala
			180					185					190		
Ser	Phe	Leu	Leu	Arg	Glu	Gly	Glu	Asp	Thr	Leu	Glu	Leu	Ala	Arg	Arg
		195					200					205			
Phe	Ser	Thr	Arg	Ser	Leu	Arg	Glu	Lys	Phe	Asp	Glu	Gly	Gly	Asp	Glu
210					215					220					
Ile	Asp	Glu	Asp	Leu	Ser	Ser	Trp	Ile	Arg	His	Ser	Leu	Asp	Leu	Pro
225				230						235					240
Leu	His	Trp	Arg	Val	Gln	Gly	Leu	Glu	Ala	Arg	Trp	Phe	Leu	Asp	Ala
				245					250					255	
Tyr	Ala	Arg	Arg	Pro	Asp	Met	Asn	Pro	Leu	Ile	Phe	Lys	Leu	Ala	Lys
			260					265					270		
Leu	Asn	Phe	Asn	Ile	Val	Gln	Ala	Thr	Tyr	Gln	Glu	Glu	Leu	Lys	Asp
		275					280					285			
Ile	Ser	Arg	Trp	Trp	Asn	Ser	Ser	Cys	Leu	Ala	Glu	Lys	Leu	Pro	Phe
290					295					300					
Val	Arg	Asp	Arg	Ile	Val	Glu	Cys	Phe	Phe	Trp	Ala	Ile	Ala	Ala	Phe
305				310					315						320
Glu	Pro	His	Gln	Tyr	Ser	Tyr	Gln	Arg	Lys	Met	Ala	Ala	Val	Ile	Ile
				325					330					335	
Thr	Phe	Ile	Thr	Ile	Ile	Asp	Asp	Val	Tyr	Asp	Val	Tyr	Gly	Thr	Ile
			340				345						350		
Glu	Glu	Leu	Glu	Leu	Leu	Thr	Asp	Met	Ile	Arg	Arg	Trp	Asp	Asn	Lys

355					360					365					
Ser	Ile	Ser	Gln	Leu	Pro	Tyr	Tyr	Met	Gln	Val	Cys	Tyr	Leu	Ala	Leu
370					375					380					
Tyr	Asn	Phe	Val	Ser	Glu	Arg	Ala	Tyr	Asp	Ile	Leu	Lys	Asp	Gln	His
385					390					395					400
Phe	Asn	Ser	Ile	Pro	Tyr	Leu	Gln	Arg	Ser	Trp	Val	Ser	Leu	Val	Glu
				405					410					415	
Gly	Tyr	Leu	Lys	Glu	Ala	Tyr	Trp	Tyr	Tyr	Asn	Gly	Tyr	Lys	Pro	Ser
			420					425					430		
Leu	Glu	Glu	Tyr	Leu	Asn	Asn	Ala	Lys	Ile	Ser	Ile	Ser	Ala	Pro	Thr
		435					440					445			
Ile	Ile	Ser	Gln	Leu	Tyr	Phe	Thr	Leu	Ala	Asn	Ser	Ile	Asp	Glu	Thr
		450				455					460				
Ala	Ile	Glu	Ser	Leu	Tyr	Gln	Tyr	His	Asn	Ile	Leu	Tyr	Leu	Ser	Gly
465				470						475					480
Thr	Ile	Leu	Arg	Leu	Ala	Asp	Asp	Leu	Gly	Thr	Ser	Gln	His	Glu	Leu
				485					490					495	
Glu	Arg	Gly	Asp	Val	Pro	Lys	Ala	Ile	Gln	Cys	Tyr	Met	Asn	Asp	Thr
			500					505					510		
Asn	Ala	Ser	Glu	Arg	Glu	Ala	Val	Glu	His	Val	Lys	Phe	Leu	Ile	Arg
			515				520					525			
Glu	Ala	Trp	Lys	Glu	Met	Asn	Thr	Val	Thr	Thr	Ala	Ser	Asp	Cys	Pro
				530			535					540			
Phe	Thr	Asp	Asp	Leu	Val	Ala	Ala	Ala	Ala	Asn	Leu	Ala	Arg	Ala	Ala
545				550						555					560
Gln	Phe	Ile	Tyr	Leu	Asp	Gly	Asp	Gly	His	Gly	Val	Gln	His	Ser	Glu
				565				570						575	
Ile	His	Gln	Gln	Met	Gly	Gly	Leu	Leu	Phe	Gln	Pro	Tyr	Val		
			580				585						590		

<210> 62

<211> 590

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

computer-generated protein sequence variant

<220>

<221> VARIANT

<222> (1)..(590)

<223> computer-generated (+)-sabinene synthase protein
sequence variant

<400> 62

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Met Ser Ser Ile Ser Ile Asn Ile Ala Met Pro Leu Asn Ser Leu His
 1           5           10           15

Asn Phe Glu Arg Lys Pro Ser Lys Ala Trp Ser Thr Ser Cys Thr Ala
      20           25           30

Pro Ala Ala Arg Leu Arg Ala Ser Ser Ser Leu Gln Gln Glu Lys Pro
      35           40           45

His Gln Ile Arg Arg Ser Gly Asp Tyr Gln Pro Ser Leu Trp Asp Phe
      50           55           60

Asn Tyr Val Gln Ser Leu Asn Thr Pro Tyr Lys Glu Gln Arg His Phe
      65           70           75           80

Asn Arg Gln Ala Glu Leu Ile Met Gln Val Arg Met Leu Leu Lys Val
      85           90           95

Lys Met Glu Ala Ile Gln Gln Leu Glu Leu Ile Asp Asp Leu Gln Tyr
      100          105          110

Leu Gly Leu Ser Tyr Phe Phe Gln Asp Glu Ile Lys Gln Ile Leu Ser
      115          120          125

Ser Ile His Asn Glu Pro Arg Tyr Phe His Asn Asn Asp Leu Tyr Phe
      130          135          140

Thr Ala Leu Gly Phe Arg Ile Leu Arg Gln His Gly Phe Asn Val Ser
      145          150          155          160

Glu Asp Val Phe Asp Cys Phe Lys Ile Glu Lys Cys Ser Asp Phe Asn
      165          170          175

Ala Asn Leu Ala Gln Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala
      180          185          190

Ser Phe Leu Leu Arg Glu Gly Glu Asp Thr Leu Glu Leu Ala Arg Arg
      195          200          205

Phe Ser Thr Arg Ser Leu Arg Glu Lys Phe Asp Glu Gly Gly Asp Glu
      210          215          220

Ile Asp Glu Asp Leu Ser Ser Trp Ile Arg His Ser Leu Asp Leu Pro
      225          230          235          240

Leu His Trp Arg Val Gln Gly Leu Glu Ala Arg Trp Phe Leu Asp Ala
      245          250          255

Tyr Ala Arg Arg Pro Asp Met Asn Pro Leu Ile Phe Lys Leu Ala Lys
      260          265          270

Leu Asn Phe Asn Ile Val Gln Ala Thr Tyr Gln Glu Glu Leu Lys Asp
      275          280          285

Ile Ser Arg Trp Trp Asn Ser Ser Cys Leu Ala Glu Lys Leu Pro Phe
      290          295          300

Val Arg Asp Arg Ile Val Glu Cys Phe Phe Trp Ala Ile Ala Ala Phe
      305          310          315          320

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Glu Pro His Gln Tyr Ser Tyr Gln Arg Lys Met Ala Ala Val Ile Ile
 325 330 335
 Thr Phe Ile Thr Ile Ile Asp Asp Val Tyr Asp Val Tyr Gly Thr Ile
 340 345 350
 Glu Glu Leu Glu Leu Leu Thr Asp Met Ile Arg Arg Trp Asp Asn Lys
 355 360 365
 Ser Ile Ser Gln Leu Pro Tyr Tyr Met Gln Val Cys Tyr Leu Ala Leu
 370 375 380
 Tyr Asn Phe Val Ser Glu Arg Ala Tyr Asp Ile Leu Lys Asp Gln His
 385 390 395 400
 Phe Asn Ser Ile Pro Tyr Leu Gln Arg Ser Trp Val Ser Leu Val Glu
 405 410 415
 Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr Tyr Asn Gly Tyr Lys Pro Ser
 420 425 430
 Leu Glu Glu Tyr Leu Asn Asn Ala Lys Ile Ser Ile Ser Ala Pro Thr
 435 440 445
 Ile Ile Ser Gln Leu Tyr Phe Thr Leu Ala Asn Ser Ile Asp Glu Thr
 450 455 460
 Ala Ile Glu Ser Leu Tyr Gln Tyr His Asn Ile Leu Tyr Leu Ser Gly
 465 470 475 480
 Thr Ile Leu Arg Leu Ala Asp Asp Leu Gly Thr Ser Gln His Glu Leu
 485 490 495
 Glu Arg Gly Asp Val Pro Lys Ala Ile Gln Cys Tyr Met Asn Asp Thr
 500 505 510
 Asn Ala Ser Glu Arg Glu Ala Val Glu His Val Lys Phe Leu Ile Arg
 515 520 525
 Glu Ala Trp Lys Glu Met Asn Thr Val Thr Thr Ala Ser Asp Cys Pro
 530 535 540
 Phe Thr Asp Asp Leu Val Ala Ala Ala Ala Asn Leu Ala Arg Ala Ala
 545 550 555 560
 Gln Phe Ile Tyr Leu Asp Gly Asp Gly His Gly Val Gln His Ser Glu
 565 570 575
 Ile His Gln Gln Met Gly Gly Leu Leu Phe Gln Pro Tyr Val
 580 585 590

<210> 63

<211> 590

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

computer-generated protein sequence

<220>

<221> VARIANT

<222> (1)..(590)

<223> computer-generated (+)-sabinene synthase protein
sequence variant

<400> 63

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20 25 30Pro Ala Ala Arg Leu Arg Ala Ser Ser Ser Leu Gln Gln Glu Lys Pro
35 40 45His Gln Ile Arg Arg Ser Gly Asp Tyr Gln Pro Ser Leu Trp Asp Phe
50 55 60Asn Tyr Ile Gln Ser Ile Asn Thr Pro Tyr Lys Glu Gln Arg His Phe
65 70 75 80Asn Arg Gln Ala Glu Leu Ile Met Gln Val Arg Met Leu Leu Lys Val
85 90 95Lys Met Glu Ala Ile Gln Gln Leu Glu Leu Ile Asp Asp Leu Gln Tyr
100 105 110Leu Gly Leu Ser Tyr Phe Phe Gln Asp Glu Ile Lys Gln Ile Leu Ser
115 120 125Ser Ile His Asn Glu Pro Arg Tyr Phe His Asn Asn Asp Leu Tyr Phe
130 135 140Thr Ala Leu Gly Phe Arg Ile Leu Arg Gln His Gly Phe Asn Val Ser
145 150 155 160Glu Asp Val Phe Asp Cys Phe Lys Ile Glu Lys Cys Ser Asp Phe Asn
165 170 175Ala Asn Leu Ala Gln Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala
180 185 190Ser Phe Leu Leu Arg Glu Gly Glu Asp Thr Leu Glu Leu Ala Arg Arg
195 200 205Phe Ser Thr Arg Ser Leu Arg Glu Lys Phe Asp Glu Gly Gly Asp Glu
210 215 220Ile Asp Glu Asp Leu Ser Ser Trp Ile Arg His Ser Leu Asp Leu Pro
225 230 235 240Leu His Trp Arg Val Gln Gly Leu Glu Ala Arg Trp Phe Leu Asp Ala
245 250 255Tyr Ala Arg Arg Pro Asp Met Asn Pro Leu Ile Phe Lys Leu Ala Lys
260 265 270

Leu Asn Phe Asn Ile Val Gln Ala Thr Tyr Gln Glu Glu Leu Lys Asp
 275 280 285
 Ile Ser Arg Trp Trp Asn Ser Ser Cys Leu Ala Glu Lys Leu Pro Phe
 290 295 300
 Val Arg Asp Arg Ile Val Glu Cys Phe Phe Trp Ala Ile Ala Ala Phe
 305 310 315 320
 Glu Pro His Gln Tyr Ser Tyr Gln Arg Lys Met Ala Ala Val Ile Ile
 325 330 335
 Thr Phe Ile Thr Ile Ile Asp Asp Val Tyr Asp Val Tyr Gly Thr Ile
 340 345 350
 Glu Glu Leu Glu Leu Leu Thr Asp Met Ile Arg Arg Trp Asp Asn Lys
 355 360 365
 Ser Ile Ser Gln Leu Pro Tyr Tyr Met Gln Val Cys Tyr Leu Ala Leu
 370 375 380
 Tyr Asn Phe Val Ser Glu Arg Ala Tyr Asp Ile Leu Lys Asp Gln His
 385 390 395 400
 Phe Asn Ser Ile Pro Tyr Leu Gln Arg Ser Trp Val Ser Leu Val Glu
 405 410 415
 Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr Tyr Asn Gly Tyr Lys Pro Ser
 420 425 430
 Leu Glu Glu Tyr Leu Asn Asn Ala Lys Ile Ser Ile Ser Ala Pro Thr
 435 440 445
 Ile Ile Ser Gln Leu Tyr Phe Thr Leu Ala Asn Ser Ile Asp Glu Thr
 450 455 460
 Ala Ile Glu Ser Leu Tyr Gln Tyr His Asn Ile Leu Tyr Leu Ser Gly
 465 470 475 480
 Thr Ile Leu Arg Leu Ala Asp Asp Leu Gly Thr Ser Gln His Glu Leu
 485 490 495
 Glu Arg Gly Asp Val Pro Lys Ala Ile Gln Cys Tyr Met Asn Asp Thr
 500 505 510
 Asn Ala Ser Glu Arg Glu Ala Val Glu His Val Lys Phe Leu Ile Arg
 515 520 525
 Glu Ala Trp Lys Glu Met Asn Thr Val Thr Thr Ala Ser Asp Cys Pro
 530 535 540
 Phe Thr Asp Asp Leu Val Ala Ala Ala Ala Asn Leu Ala Arg Ala Ala
 545 550 555 560
 Gln Phe Ile Tyr Leu Asp Gly Asp Gly His Gly Val Gln His Ser Glu
 565 570 575
 Ile His Gln Gln Met Gly Gly Leu Leu Phe Gln Pro Tyr Val
 580 585 590

<210> 64
 <211> 590
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 computer-generated protein sequence

<220>
 <221> VARIANT
 <222> (1)..(590)
 <223> computer-generated (+)-sabinene synthase protein
 sequence variant

<400> 64
 Met Ser Ser Ile Ser Ile Asn Ile Ala Met Pro Leu Asn Ser Leu His
 1 5 10 15
 Asn Phe Glu Arg Lys Pro Ser Lys Ala Trp Ser Thr Ser Cys Thr Ala
 20 25 30
 Pro Ala Ala Arg Leu Arg Ala Ser Ser Ser Leu Gln Gln Glu Lys Pro
 35 40 45
 His Gln Ile Arg Arg Ser Gly Asp Tyr Gln Pro Ser Leu Trp Asp Phe
 50 55 60
 Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Lys Glu Gln Arg His Phe
 65 70 75 80
 Asn Arg Gln Ala Glu Val Ile Met Gln Val Arg Met Leu Leu Lys Val
 85 90 95
 Lys Met Glu Ala Ile Gln Gln Leu Glu Leu Ile Asp Asp Leu Gln Tyr
 100 105 110
 Leu Gly Leu Ser Tyr Phe Phe Gln Asp Glu Ile Lys Gln Ile Leu Ser
 115 120 125
 Ser Ile His Asn Glu Pro Arg Tyr Phe His Asn Asn Asp Leu Tyr Phe
 130 135 140
 Thr Ala Leu Gly Phe Arg Ile Leu Arg Gln His Gly Phe Asn Val Ser
 145 150 155 160
 Glu Asp Val Phe Asp Cys Phe Lys Ile Glu Lys Cys Ser Asp Phe Asn
 165 170 175
 Ala Asn Leu Ala Gln Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala
 180 185 190
 Ser Phe Leu Leu Arg Glu Gly Glu Asp Thr Leu Glu Leu Ala Arg Arg
 195 200 205
 Phe Ser Thr Arg Ser Leu Arg Glu Lys Phe Asp Glu Gly Gly Asp Glu
 210 215 220
 Ile Asp Glu Asp Leu Ser Ser Trp Ile Arg His Ser Leu Asp Leu Pro

225	230	235	240
Leu His Trp Arg	Val Gln Gly Leu Glu Ala Arg Trp Phe Leu Asp Ala		
	245	250	255
Tyr Ala Arg Arg	Pro Asp Met Asn Pro Leu Ile Phe Lys Leu Ala Lys		
	260	265	270
Leu Asn Phe Asn Ile Val Gln Ala Thr Tyr Gln Glu Glu Leu Lys Asp			
	275	280	285
Ile Ser Arg Trp Trp Asn Ser Ser Cys Leu Ala Glu Lys Leu Pro Phe			
	290	295	300
Val Arg Asp Arg Ile Val Glu Cys Phe Phe Trp Ala Ile Ala Ala Phe			
305	310	315	320
Glu Pro His Gln Tyr Ser Tyr Gln Arg Lys Met Ala Ala Val Ile Ile			
	325	330	335
Thr Phe Ile Thr Ile Ile Asp Asp Val Tyr Asp Val Tyr Gly Thr Ile			
	340	345	350
Glu Glu Leu Glu Leu Leu Thr Asp Met Ile Arg Arg Trp Asp Asn Lys			
	355	360	365
Ser Ile Ser Gln Leu Pro Tyr Tyr Met Gln Val Cys Tyr Leu Ala Leu			
	370	375	380
Tyr Asn Phe Val Ser Glu Arg Ala Tyr Asp Ile Leu Lys Asp Gln His			
385	390	395	400
Phe Asn Ser Ile Pro Tyr Leu Gln Arg Ser Trp Val Ser Leu Val Glu			
	405	410	415
Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr Tyr Asn Gly Tyr Lys Pro Ser			
	420	425	430
Leu Glu Glu Tyr Leu Asn Asn Ala Lys Ile Ser Ile Ser Ala Pro Thr			
	435	440	445
Ile Ile Ser Gln Leu Tyr Phe Thr Leu Ala Asn Ser Ile Asp Glu Thr			
	450	455	460
Ala Ile Glu Ser Leu Tyr Gln Tyr His Asn Ile Leu Tyr Leu Ser Gly			
465	470	475	480
Thr Ile Leu Arg Leu Ala Asp Asp Leu Gly Thr Ser Gln His Glu Leu			
	485	490	495
Glu Arg Gly Asp Val Pro Lys Ala Ile Gln Cys Tyr Met Asn Asp Thr			
	500	505	510
Asn Ala Ser Glu Arg Glu Ala Val Glu His Val Lys Phe Leu Ile Arg			
	515	520	525
Glu Ala Trp Lys Glu Met Asn Thr Val Thr Thr Ala Ser Asp Cys Pro			
	530	535	540
Phe Thr Asp Asp Leu Val Ala Ala Ala Ala Asn Leu Ala Arg Ala Ala			

545				550				555				560			
Gln	Phe	Ile	Tyr	Leu 565	Asp	Gly	Asp	Gly	His 570	Gly	Val	Gln	His	Ser 575	Glu
Ile	His	Gln	Gln 580	Met	Gly	Gly	Leu	Leu 585	Phe	Gln	Pro	Tyr	Val 590		

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<210> 65
<211> 590
<212> PRT
<213> Artificial Sequence
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<223> Description of Artificial Sequence:
computer-generated protein sequence

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<220>
<221> VARIANT
<222> (1)..(590)
<223> computer-generated (+)-sabinene synthase protein
sequence variant
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Asn	Phe	Glu	Arg	Lys	Pro	Ser	Lys	Ala	Trp	Ser	Thr	Ser	Cys	Thr	Ala		
			20					25					30				
Pro	Ala	Ala	Arg	Leu	Arg	Ala	Ser	Ser	Ser	Leu	Gln	Gln	Glu	Lys	Pro		
		35					40					45					
His	Gln	Ile	Arg	Arg	Ser	Gly	Asp	Tyr	Gln	Pro	Ser	Leu	Trp	Asp	Phe		
	50					55					60						
Asn	Tyr	Ile	Gln	Ser	Leu	Asn	Thr	Pro	Tyr	Lys	Glu	Gln	Arg	His	Phe		
65					70					75					80		
Asn	Arg	Gln	Ala	Glu	Leu	Ile	Met	Gln	Val	Arg	Met	Leu	Leu	Lys	Val		
				85					90					95			
Lys	Met	Glu	Ala	Leu	Gln	Gln	Leu	Glu	Leu	Ile	Asp	Asp	Leu	Gln	Tyr		
			100					105					110				
Leu	Gly	Leu	Ser	Tyr	Phe	Phe	Gln	Asp	Glu	Ile	Lys	Gln	Ile	Leu	Ser		
	115						120					125					
Ser	Ile	His	Asn	Glu	Pro	Arg	Tyr	Phe	His	Asn	Asn	Asp	Leu	Tyr	Phe		
	130					135					140						
Thr	Ala	Leu	Gly	Phe	Arg	Ile	Leu	Arg	Gln	His	Gly	Phe	Asn	Val	Ser		
145					150					155					160		
Glu	Asp	Val	Phe	Asp	Cys	Phe	Lys	Ile	Glu	Lys	Cys	Ser	Asp	Phe	Asn		
				165					170					175			
Ala	Asn	Leu	Ala	Gln	Asp	Thr	Lys	Gly	Met	Leu	Gln	Leu	Tyr	Glu	Ala		
			180					185					190				

Ser Phe Leu Leu Arg Glu Gly Glu Asp Thr Leu Glu Leu Ala Arg Arg
 195 200 205
 Phe Ser Thr Arg Ser Leu Arg Glu Lys Phe Asp Glu Gly Gly Asp Glu
 210 215 220
 Ile Asp Glu Asp Leu Ser Ser Trp Ile Arg His Ser Leu Asp Leu Pro
 225 230 235 240
 Leu His Trp Arg Val Gln Gly Leu Glu Ala Arg Trp Phe Leu Asp Ala
 245 250 255
 Tyr Ala Arg Arg Pro Asp Met Asn Pro Leu Ile Phe Lys Leu Ala Lys
 260 265 270
 Leu Asn Phe Asn Ile Val Gln Ala Thr Tyr Gln Glu Glu Leu Lys Asp
 275 280 285
 Ile Ser Arg Trp Trp Asn Ser Ser Cys Leu Ala Glu Lys Leu Pro Phe
 290 295 300
 Val Arg Asp Arg Ile Val Glu Cys Phe Phe Trp Ala Ile Ala Ala Phe
 305 310 315 320
 Glu Pro His Gln Tyr Ser Tyr Gln Arg Lys Met Ala Ala Val Ile Ile
 325 330 335
 Thr Phe Ile Thr Ile Ile Asp Asp Val Tyr Asp Val Tyr Gly Thr Ile
 340 345 350
 Glu Glu Leu Glu Leu Leu Thr Asp Met Ile Arg Arg Trp Asp Asn Lys
 355 360 365
 Ser Ile Ser Gln Leu Pro Tyr Tyr Met Gln Val Cys Tyr Leu Ala Leu
 370 375 380
 Tyr Asn Phe Val Ser Glu Arg Ala Tyr Asp Ile Leu Lys Asp Gln His
 385 390 395 400
 Phe Asn Ser Ile Pro Tyr Leu Gln Arg Ser Trp Val Ser Leu Val Glu
 405 410 415
 Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr Tyr Asn Gly Tyr Lys Pro Ser
 420 425 430
 Leu Glu Glu Tyr Leu Asn Asn Ala Lys Ile Ser Ile Ser Ala Pro Thr
 435 440 445
 Ile Ile Ser Gln Leu Tyr Phe Thr Leu Ala Asn Ser Ile Asp Glu Thr
 450 455 460
 Ala Ile Glu Ser Leu Tyr Gln Tyr His Asn Ile Leu Tyr Leu Ser Gly
 465 470 475 480
 Thr Ile Leu Arg Leu Ala Asp Asp Leu Gly Thr Ser Gln His Glu Leu
 485 490 495
 Glu Arg Gly Asp Val Pro Lys Ala Ile Gln Cys Tyr Met Asn Asp Thr
 500 505 510

Asn Ala Ser Glu Arg Glu Ala Val Glu His Val Lys Phe Leu Ile Arg
 515 520 525

Glu Ala Trp Lys Glu Met Asn Thr Val Thr Thr Ala Ser Asp Cys Pro
 530 535 540

Phe Thr Asp Asp Leu Val Ala Ala Ala Ala Asn Leu Ala Arg Ala Ala
 545 550 555 560

Gln Phe Ile Tyr Leu Asp Gly Asp Gly His Gly Val Gln His Ser Glu
 565 570 575

Ile His Gln Gln Met Gly Gly Leu Leu Phe Gln Pro Tyr Val
 580 585 590

<210> 66

<211> 590

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 computer-generated protein sequence

<220>

<221> VARIANT

<222> (1)..(590)

<223> computer-generated (+)-sabinene synthase protein
 sequence variant

<400> 66

Met Ser Ser Ile Ser Ile Asn Ile Ala Met Pro Leu Asn Ser Leu His
 1 5 10 15

Asn Phe Glu Arg Lys Pro Ser Lys Ala Trp Ser Thr Ser Cys Thr Ala
 20 25 30

Pro Ala Ala Arg Leu Arg Ala Ser Ser Ser Leu Gln Gln Glu Lys Pro
 35 40 45

His Gln Ile Arg Arg Ser Gly Asp Tyr Gln Pro Ser Leu Trp Asp Phe
 50 55 60

Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Lys Glu Gln Arg His Phe
 65 70 75 80

Asn Arg Gln Ala Glu Leu Ile Met Gln Val Arg Met Leu Leu Lys Val
 85 90 95

Lys Met Glu Ala Ile Gln Gln Val Glu Leu Ile Asp Asp Leu Gln Tyr
 100 105 110

Leu Gly Leu Ser Tyr Phe Phe Gln Asp Glu Ile Lys Gln Ile Leu Ser
 115 120 125

Ser Ile His Asn Glu Pro Arg Tyr Phe His Asn Asn Asp Leu Tyr Phe
 130 135 140

Thr Ala Leu Gly Phe Arg Ile Leu Arg Gln His Gly Phe Asn Val Ser
 145 150 155 160
 Glu Asp Val Phe Asp Cys Phe Lys Ile Glu Lys Cys Ser Asp Phe Asn
 165 170 175
 Ala Asn Leu Ala Gln Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala
 180 185 190
 Ser Phe Leu Leu Arg Glu Gly Glu Asp Thr Leu Glu Leu Ala Arg Arg
 195 200 205
 Phe Ser Thr Arg Ser Leu Arg Glu Lys Phe Asp Glu Gly Gly Asp Glu
 210 215 220
 Ile Asp Glu Asp Leu Ser Ser Trp Ile Arg His Ser Leu Asp Leu Pro
 225 230 235 240
 Leu His Trp Arg Val Gln Gly Leu Glu Ala Arg Trp Phe Leu Asp Ala
 245 250 255
 Tyr Ala Arg Arg Pro Asp Met Asn Pro Leu Ile Phe Lys Leu Ala Lys
 260 265 270
 Leu Asn Phe Asn Ile Val Gln Ala Thr Tyr Gln Glu Glu Leu Lys Asp
 275 280 285
 Ile Ser Arg Trp Trp Asn Ser Ser Cys Leu Ala Glu Lys Leu Pro Phe
 290 295 300
 Val Arg Asp Arg Ile Val Glu Cys Phe Phe Trp Ala Ile Ala Ala Phe
 305 310 315 320
 Glu Pro His Gln Tyr Ser Tyr Gln Arg Lys Met Ala Ala Val Ile Ile
 325 330 335
 Thr Phe Ile Thr Ile Ile Asp Asp Val Tyr Asp Val Tyr Gly Thr Ile
 340 345 350
 Glu Glu Leu Glu Leu Leu Thr Asp Met Ile Arg Arg Trp Asp Asn Lys
 355 360 365
 Ser Ile Ser Gln Leu Pro Tyr Tyr Met Gln Val Cys Tyr Leu Ala Leu
 370 375 380
 Tyr Asn Phe Val Ser Glu Arg Ala Tyr Asp Ile Leu Lys Asp Gln His
 385 390 395 400
 Phe Asn Ser Ile Pro Tyr Leu Gln Arg Ser Trp Val Ser Leu Val Glu
 405 410 415
 Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr Tyr Asn Gly Tyr Lys Pro Ser
 420 425 430
 Leu Glu Glu Tyr Leu Asn Asn Ala Lys Ile Ser Ile Ser Ala Pro Thr
 435 440 445
 Ile Ile Ser Gln Leu Tyr Phe Thr Leu Ala Asn Ser Ile Asp Glu Thr
 450 455 460

Ala Ile Glu Ser Leu Tyr Gln Tyr His Asn Ile Leu Tyr Leu Ser Gly
 465 470 475 480
 Thr Ile Leu Arg Leu Ala Asp Asp Leu Gly Thr Ser Gln His Glu Leu
 485 490 495
 Glu Arg Gly Asp Val Pro Lys Ala Ile Gln Cys Tyr Met Asn Asp Thr
 500 505 510
 Asn Ala Ser Glu Arg Glu Ala Val Glu His Val Lys Phe Leu Ile Arg
 515 520 525
 Glu Ala Trp Lys Glu Met Asn Thr Val Thr Thr Ala Ser Asp Cys Pro
 530 535 540
 Phe Thr Asp Asp Leu Val Ala Ala Ala Ala Asn Leu Ala Arg Ala Ala
 545 550 555 560
 Gln Phe Ile Tyr Leu Asp Gly Asp Gly His Gly Val Gln His Ser Glu
 565 570 575
 Ile His Gln Gln Met Gly Gly Leu Leu Phe Gln Pro Tyr Val
 580 585 590

<210> 67

<211> 590

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
computer-generated protein sequence

<220>

<221> VARIANT

<222> (1)..(590)

<223> computer-generated (+)-sabinene synthase protein
sequence variant

<400> 67

Met Ser Ser Ile Ser Ile Asn Ile Ala Met Pro Leu Asn Ser Leu His
 1 5 10 15
 Asn Phe Glu Arg Lys Pro Ser Lys Ala Trp Ser Thr Ser Cys Thr Ala
 20 25 30
 Pro Ala Ala Arg Leu Arg Ala Ser Ser Ser Leu Gln Gln Glu Lys Pro
 35 40 45
 His Gln Ile Arg Arg Ser Gly Asp Tyr Gln Pro Ser Leu Trp Asp Phe
 50 55 60
 Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Lys Glu Gln Arg His Phe
 65 70 75 80
 Asn Arg Gln Ala Glu Leu Ile Met Gln Val Arg Met Leu Leu Lys Val
 85 90 95
 Lys Met Glu Ala Ile Gln Gln Leu Glu Val Ile Asp Asp Leu Gln Tyr

100	105	110
Leu Gly Leu Ser Tyr Phe Phe Gln Asp Glu Ile Lys Gln Ile Leu Ser 115 120 125		
Ser Ile His Asn Glu Pro Arg Tyr Phe His Asn Asn Asp Leu Tyr Phe 130 135 140		
Thr Ala Leu Gly Phe Arg Ile Leu Arg Gln His Gly Phe Asn Val Ser 145 150 155 160		
Glu Asp Val Phe Asp Cys Phe Lys Ile Glu Lys Cys Ser Asp Phe Asn 165 170 175		
Ala Asn Leu Ala Gln Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala 180 185 190		
Ser Phe Leu Leu Arg Glu Gly Glu Asp Thr Leu Glu Leu Ala Arg Arg 195 200 205		
Phe Ser Thr Arg Ser Leu Arg Glu Lys Phe Asp Glu Gly Gly Asp Glu 210 215 220		
Ile Asp Glu Asp Leu Ser Ser Trp Ile Arg His Ser Leu Asp Leu Pro 225 230 235 240		
Leu His Trp Arg Val Gln Gly Leu Glu Ala Arg Trp Phe Leu Asp Ala 245 250 255		
Tyr Ala Arg Arg Pro Asp Met Asn Pro Leu Ile Phe Lys Leu Ala Lys 260 265 270		
Leu Asn Phe Asn Ile Val Gln Ala Thr Tyr Gln Glu Glu Leu Lys Asp 275 280 285		
Ile Ser Arg Trp Trp Asn Ser Ser Cys Leu Ala Glu Lys Leu Pro Phe 290 295 300		
Val Arg Asp Arg Ile Val Glu Cys Phe Phe Trp Ala Ile Ala Ala Phe 305 310 315 320		
Glu Pro His Gln Tyr Ser Tyr Gln Arg Lys Met Ala Ala Val Ile Ile 325 330 335		
Thr Phe Ile Thr Ile Ile Asp Asp Val Tyr Asp Val Tyr Gly Thr Ile 340 345 350		
Glu Glu Leu Glu Leu Leu Thr Asp Met Ile Arg Arg Trp Asp Asn Lys 355 360 365		
Ser Ile Ser Gln Leu Pro Tyr Tyr Met Gln Val Cys Tyr Leu Ala Leu 370 375 380		
Tyr Asn Phe Val Ser Glu Arg Ala Tyr Asp Ile Leu Lys Asp Gln His 385 390 395 400		
Phe Asn Ser Ile Pro Tyr Leu Gln Arg Ser Trp Val Ser Leu Val Glu 405 410 415		
Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr Tyr Asn Gly Tyr Lys Pro Ser		

420	425	430
Leu Glu Glu Tyr Leu Asn Asn Ala Lys Ile Ser Ile Ser Ala Pro Thr		
435	440	445
Ile Ile Ser Gln Leu Tyr Phe Thr Leu Ala Asn Ser Ile Asp Glu Thr		
450	455	460
Ala Ile Glu Ser Leu Tyr Gln Tyr His Asn Ile Leu Tyr Leu Ser Gly		
465	470	475
Thr Ile Leu Arg Leu Ala Asp Asp Leu Gly Thr Ser Gln His Glu Leu		
485	490	495
Glu Arg Gly Asp Val Pro Lys Ala Ile Gln Cys Tyr Met Asn Asp Thr		
500	505	510
Asn Ala Ser Glu Arg Glu Ala Val Glu His Val Lys Phe Leu Ile Arg		
515	520	525
Glu Ala Trp Lys Glu Met Asn Thr Val Thr Thr Ala Ser Asp Cys Pro		
530	535	540
Phe Thr Asp Asp Leu Val Ala Ala Ala Asn Leu Ala Arg Ala Ala		
545	550	555
Gln Phe Ile Tyr Leu Asp Gly Asp Gly His Gly Val Gln His Ser Glu		
565	570	575
Ile His Gln Gln Met Gly Gly Leu Leu Phe Gln Pro Tyr Val		
580	585	590

<210> 68

<211> 590

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
computer-generated protein sequence

<220>

<221> VARIANT

<222> (1)..(590)

<223> computer-generated (+)-sabinene synthase protein
sequence variant

<400> 68

Met Ser Ser Ile Ser Ile Asn Ile Ala Met Pro Leu Asn Ser Leu His
1 5 10 15

Asn Phe Glu Arg Lys Pro Ser Lys Ala Trp Ser Thr Ser Cys Thr Ala
20 25 30

Pro Ala Ala Arg Leu Arg Ala Ser Ser Ser Leu Gln Gln Glu Lys Pro
35 40 45

His Gln Ile Arg Arg Ser Gly Asp Tyr Gln Pro Ser Leu Trp Asp Phe
50 55 60

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Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Lys Glu Gln Arg His Phe
 65                               70                               75                               80

Asn Arg Gln Ala Glu Leu Ile Met Gln Val Arg Met Leu Leu Lys Val
                               85                               90                               95

Lys Met Glu Ala Ile Gln Gln Leu Glu Leu Ile Asp Asp Val Gln Tyr
                100                105                110

Leu Gly Leu Ser Tyr Phe Phe Gln Asp Glu Ile Lys Gln Ile Leu Ser
    115                120                125

Ser Ile His Asn Glu Pro Arg Tyr Phe His Asn Asn Asp Leu Tyr Phe
    130                135                140

Thr Ala Leu Gly Phe Arg Ile Leu Arg Gln His Gly Phe Asn Val Ser
145                150                155                160

Glu Asp Val Phe Asp Cys Phe Lys Ile Glu Lys Cys Ser Asp Phe Asn
                165                170                175

Ala Asn Leu Ala Gln Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala
    180                185                190

Ser Phe Leu Leu Arg Glu Gly Glu Asp Thr Leu Glu Leu Ala Arg Arg
    195                200                205

Phe Ser Thr Arg Ser Leu Arg Glu Lys Phe Asp Glu Gly Gly Asp Glu
    210                215                220

Ile Asp Glu Asp Leu Ser Ser Trp Ile Arg His Ser Leu Asp Leu Pro
225                230                235                240

Leu His Trp Arg Val Gln Gly Leu Glu Ala Arg Trp Phe Leu Asp Ala
    245                250                255

Tyr Ala Arg Arg Pro Asp Met Asn Pro Leu Ile Phe Lys Leu Ala Lys
    260                265                270

Leu Asn Phe Asn Ile Val Gln Ala Thr Tyr Gln Glu Glu Leu Lys Asp
    275                280                285

Ile Ser Arg Trp Trp Asn Ser Ser Cys Leu Ala Glu Lys Leu Pro Phe
    290                295                300

Val Arg Asp Arg Ile Val Glu Cys Phe Phe Trp Ala Ile Ala Ala Phe
305                310                315                320

Glu Pro His Gln Tyr Ser Tyr Gln Arg Lys Met Ala Ala Val Ile Ile
    325                330                335

Thr Phe Ile Thr Ile Ile Asp Asp Val Tyr Asp Val Tyr Gly Thr Ile
    340                345                350

Glu Glu Leu Glu Leu Leu Thr Asp Met Ile Arg Arg Trp Asp Asn Lys
    355                360                365

Ser Ile Ser Gln Leu Pro Tyr Tyr Met Gln Val Cys Tyr Leu Ala Leu
    370                375                380

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Tyr Asn Phe Val Ser Glu Arg Ala Tyr Asp Ile Leu Lys Asp Gln His
 385 390 395 400
 Phe Asn Ser Ile Pro Tyr Leu Gln Arg Ser Trp Val Ser Leu Val Glu
 405 410 415
 Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr Tyr Asn Gly Tyr Lys Pro Ser
 420 425 430
 Leu Glu Glu Tyr Leu Asn Asn Ala Lys Ile Ser Ile Ser Ala Pro Thr
 435 440 445
 Ile Ile Ser Gln Leu Tyr Phe Thr Leu Ala Asn Ser Ile Asp Glu Thr
 450 455 460
 Ala Ile Glu Ser Leu Tyr Gln Tyr His Asn Ile Leu Tyr Leu Ser Gly
 465 470 475 480
 Thr Ile Leu Arg Leu Ala Asp Asp Leu Gly Thr Ser Gln His Glu Leu
 485 490 495
 Glu Arg Gly Asp Val Pro Lys Ala Ile Gln Cys Tyr Met Asn Asp Thr
 500 505 510
 Asn Ala Ser Glu Arg Glu Ala Val Glu His Val Lys Phe Leu Ile Arg
 515 520 525
 Glu Ala Trp Lys Glu Met Asn Thr Val Thr Thr Ala Ser Asp Cys Pro
 530 535 540
 Phe Thr Asp Asp Leu Val Ala Ala Ala Asn Leu Ala Arg Ala Ala
 545 550 555 560
 Gln Phe Ile Tyr Leu Asp Gly Asp Gly His Gly Val Gln His Ser Glu
 565 570 575
 Ile His Gln Gln Met Gly Gly Leu Leu Phe Gln Pro Tyr Val
 580 585 590

<210> 69

<211> 590

<212> PRT

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:
 computer-generated protein sequence

<220>

<221> VARIANT

<222> (1)..(590)

 <223> computer-generated(+)-sabinene synthase protein
 sequence

<400> 69

Met Ser Ser Ile Ser Ile Asn Ile Ala Met Pro Leu Asn Ser Leu His
 1 5 10 15

- 145 -

Thr Phe Ile Thr Ile Ile Asp Asp Val Tyr Asp Val Tyr Gly Thr Ile
 340 345 350
 Glu Glu Leu Glu Leu Leu Thr Asp Met Ile Arg Arg Trp Asp Asn Lys
 355 360 365
 Ser Ile Ser Gln Leu Pro Tyr Tyr Met Gln Val Cys Tyr Leu Ala Leu
 370 375 380
 Tyr Asn Phe Val Ser Glu Arg Ala Tyr Asp Ile Leu Lys Asp Gln His
 385 390 395 400
 Phe Asn Ser Ile Pro Tyr Leu Gln Arg Ser Trp Val Ser Leu Val Glu
 405 410 415
 Gly Tyr Leu Lys Glu Ala Tyr Trp Tyr Tyr Asn Gly Tyr Lys Pro Ser
 420 425 430
 Leu Glu Glu Tyr Leu Asn Asn Ala Lys Ile Ser Ile Ser Ala Pro Thr
 435 440 445
 Ile Ile Ser Gln Leu Tyr Phe Thr Leu Ala Asn Ser Ile Asp Glu Thr
 450 455 460
 Ala Ile Glu Ser Leu Tyr Gln Tyr His Asn Ile Leu Tyr Leu Ser Gly
 465 470 475 480
 Thr Ile Leu Arg Leu Ala Asp Asp Leu Gly Thr Ser Gln His Glu Leu
 485 490 495
 Glu Arg Gly Asp Val Pro Lys Ala Ile Gln Cys Tyr Met Asn Asp Thr
 500 505 510
 Asn Ala Ser Glu Arg Glu Ala Val Glu His Val Lys Phe Leu Ile Arg
 515 520 525
 Glu Ala Trp Lys Glu Met Asn Thr Val Thr Thr Ala Ser Asp Cys Pro
 530 535 540
 Phe Thr Asp Asp Leu Val Ala Ala Ala Ala Asn Leu Ala Arg Ala Ala
 545 550 555 560
 Gln Phe Ile Tyr Leu Asp Gly Asp Gly His Gly Val Gln His Ser Glu
 565 570 575
 Ile His Gln Gln Met Gly Gly Leu Leu Phe Gln Pro Tyr Val
 580 585 590

<210> 70

<211> 1967

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 computer-generated nucleic acid sequence

<220>

<221> CDS

<222> (13)..(1785)

<223> computer-generated nucleic acid sequence encoding
1,8-cineole synthase

<400> 70

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gatcaccaca ag atg tcg agt ctt ata atg caa gtt gtt att cct aag cca 51
      Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro
        1             5             10

gcc aaa att ttt cac aat aac tta ttc agc gtg att tca aaa cga cat 99
Ala Lys Ile Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His
  15             20             25

cgt ttc agt act aca atc acc act cgt ggt ggc agg tgg gca cat tgc 147
Arg Phe Ser Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys
  30             35             40             45

tca cta caa atg ggt aat gag atc caa act gga cga cga act gga ggc 195
Ser Leu Gln Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly
      50             55             60

tac cag cct acc att tgg gat ttc agc acc att caa ttg ttc gac tct 243
Tyr Gln Pro Thr Ile Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser
      65             70             75

gag tat aag gaa gag aag cac ttg atg agg gcc gca ggt atg ata gcc 291
Glu Tyr Lys Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala
      80             85             90

caa gtg aat atg ttg ttg cag gaa gaa gta gat tcg att caa cgg ttg 339
Gln Val Asn Met Leu Leu Gln Glu Glu Val Asp Ser Ile Gln Arg Leu
      95             100             105

gag ttg att gat gac cta cga agg ctg ggt ata tct tgc cat ttt gac 387
Glu Leu Ile Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp
  110             115             120             125

cgc gag atc gtt gaa ata tta aac tca aaa tat tat acc aac aat gag 435
Arg Glu Ile Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu
      130             135             140

ata gat gaa agt gat cta tac tca aca gcc ctt aga ttc aag ctc cta 483
Ile Asp Glu Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu
      145             150             155

aga caa tac gat ttt agc gtc tct caa gag gta ttt gat tgt ttc aag 531
Arg Gln Tyr Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys
      160             165             170

aat gac aag ggt act gat ttc aag cca agc cta gtc gat gat act aga 579
Asn Asp Lys Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg
      175             180             185

gga ttg tta caa ttg tac gaa gct tcg ttt tta tca gca caa ggc gaa 627
Gly Leu Leu Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu
  190             195             200             205

gaa acc cta cat ctt gcc aga gat ttt gct act aaa ttt ctg cat aaa 675
Glu Thr Leu His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys
      210             215             220

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aga gta cta gtt gat aaa gac att aat ctc tta tca tca att gaa cgt	723
Arg Val Leu Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg	
225 230 235	
gcg ttg gag ttg cct act cat tgg agg gtt caa atg ccc aac gca aga	771
Ala Leu Glu Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg	
240 245 250	
tcc ttc att gat gct tat aag agg aga ccc gac atg aat ccg act gtg	819
Ser Phe Ile Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val	
255 260 265	
cta gaa cta gct aaa ttg gac ttc aat atg gtt caa gca caa ttt caa	867
Leu Glu Leu Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln	
270 275 280 285	
caa gag ctc aaa gag gcc tct agg tgg tgg aat agt acg ggt ctt gtc	915
Gln Glu Leu Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val	
290 295 300	
cac gag ctt ccc ttt gtg aga gat agg att gtg gaa tgc tac tac tgg	963
His Glu Leu Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp	
305 310 315	
acg aca gga gtg gtt gag cgt cgt gaa cat gga tac gag agg ata atg	1011
Thr Thr Gly Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met	
320 325 330	
ctc acc aaa ata aat gct ctt gtt aca aca ata gac gat gtc ttt gat	1059
Leu Thr Lys Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp	
335 340 345	
att tat ggt acg ctt gaa gag cta caa cta ttc aca act gct att caa	1107
Ile Tyr Gly Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln	
350 355 360 365	
aga tgg gat att gaa tca atg aag caa ctc cct cct tac atg caa ata	1155
Arg Trp Asp Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile	
370 375 380	
tgt tat ctt gct ctc ttc aac ttt gtg aat gag atg gct tat gat act	1203
Cys Tyr Leu Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr	
385 390 395	
ctt agg gat aaa ggt ttc aac tcc acc cca tat cta cga aaa gcg tgg	1251
Leu Arg Asp Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp	
400 405 410	
gtt gat ttg gtt gag tca tat cta ata gag gca aag tgg tac tac atg	1299
Val Asp Leu Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met	
415 420 425	
gga cat aaa cct agt ttg gaa gaa tat atg aag aat agt tgg ata tca	1347
Gly His Lys Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser	
430 435 440 445	
atc gga ggc atc ccc att cta tct cat cta ttt ttc cgg cta aca gat	1395
Ile Gly Gly Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp	
450 455 460	

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tcg att gag gaa gag gat gct gag agt atg cat aaa tac cat gat att 1443
Ser Ile Glu Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile
          465                      470                      475

gtt cgt gca tcg tgt act att cta agg ctt gct gat gat atg gga aca 1491
Val Arg Ala Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr
          480                      485                      490

tcg ctg gat gag gtg gag aga ggc gac gtg ccc aaa tca gtt cag tgc 1539
Ser Leu Asp Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys
          495                      500                      505

tac atg aat gag aag aat gct tcg gaa gaa gaa gcg cga gag cat gtg 1587
Tyr Met Asn Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val
510                      515                      520                      525

cga tca ctc ata gac caa aca tgg aag atg atg aac aag gaa atg atg 1635
Arg Ser Leu Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met
          530                      535                      540

acg tca tca ttt tcc aaa tat ttt gta caa gtt tct gct aat ctt gca 1683
Thr Ser Ser Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala
          545                      550                      555

aga atg gcg caa tgg ata tac cag cat gaa tct gat gga ttt ggc atg 1731
Arg Met Ala Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met
          560                      565                      570

caa cat tca ttg gtg aac aaa atg ctc aga ggg ttg ttg ttc gac cgc 1779
Gln His Ser Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg
          575                      580                      585

tat gag taactaatct tcgcccgggt tccaaatgaa tcaatctggt gtgttgctgt 1835
Tyr Glu
590

tccacctgat atcaataata attagacaaa tgtttctgta cgggtggccc aaccgtcagg 1895

cccatttcgc tcatgttcat aataaataat aaaactgtta atcaataaca aaaaaaaaaa 1955

aaaaaaaaaa aa 1967

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<210> 71
 <211> 591
 <212> PRT
 <213> Artificial Sequence

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<400> 71
Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro Ala Lys Ile
  1                      5                      10                      15

Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His Arg Phe Ser
          20                      25                      30

Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys Ser Leu Gln
          35                      40                      45

Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro

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50					55					60					
Thr 65	Ile	Trp	Asp	Phe	Ser 70	Thr	Ile	Gln	Leu	Phe 75	Asp	Ser	Glu	Tyr	Lys 80
Glu	Glu	Lys	His	Leu 85	Met	Arg	Ala	Ala	Gly 90	Met	Ile	Ala	Gln	Val 95	Asn
Met	Leu	Leu	Gln 100	Glu	Glu	Val	Asp	Ser 105	Ile	Gln	Arg	Leu	Glu 110	Leu	Ile
Asp	Asp	Leu 115	Arg	Arg	Leu	Gly	Ile 120	Ser	Cys	His	Phe 125	Asp	Arg	Glu	Ile
Val 130	Glu	Ile	Leu	Asn	Ser	Lys 135	Tyr	Tyr	Thr	Asn 140	Asn	Glu	Ile	Asp	Glu
Ser 145	Asp	Leu	Tyr	Ser	Thr 150	Ala	Leu	Arg	Phe	Lys 155	Leu	Leu	Arg	Gln	Tyr 160
Asp	Phe	Ser	Val 165	Ser	Gln	Glu	Val	Phe 170	Asp	Cys	Phe	Lys	Asn	Asp 175	Lys
Gly	Thr	Asp	Phe 180	Lys	Pro	Ser	Leu	Val 185	Asp	Asp	Thr	Arg	Gly 190	Leu	Leu
Gln	Leu	Tyr 195	Glu	Ala	Ser	Phe	Leu 200	Ser	Ala	Gln	Gly	Glu 205	Glu	Thr	Leu
His 210	Leu	Ala	Arg	Asp	Phe	Ala 215	Thr	Lys	Phe	Leu 220	His	Lys	Arg	Val	Leu
Val 225	Asp	Lys	Asp	Ile 230	Asn	Leu	Leu	Ser	Ser 235	Ile	Glu	Arg	Ala	Leu	Glu 240
Leu	Pro	Thr	His 245	Trp	Arg	Val	Gln	Met	Pro 250	Asn	Ala	Arg	Ser	Phe 255	Ile
Asp	Ala	Tyr	Lys 260	Arg	Arg	Pro	Asp	Met 265	Asn	Pro	Thr	Val	Leu 270	Glu	Leu
Ala	Lys	Leu 275	Asp	Phe	Asn	Met	Val 280	Gln	Ala	Gln	Phe	Gln 285	Gln	Glu	Leu
Lys 290	Glu	Ala	Ser	Arg	Trp	Trp 295	Asn	Ser	Thr	Gly	Leu 300	Val	His	Glu	Leu
Pro 305	Phe	Val	Arg	Asp 310	Arg	Ile	Val	Glu	Cys	Tyr 315	Tyr	Trp	Thr	Thr	Gly 320
Val	Val	Glu	Arg	Arg 325	Glu	His	Gly	Tyr	Glu 330	Arg	Ile	Met	Leu 335	Thr	Lys
Ile	Asn	Ala 340	Leu	Val	Thr	Thr	Ile	Asp 345	Asp	Val	Phe	Asp	Ile 350	Tyr	Gly
Thr 355	Leu	Glu	Glu	Leu	Gln	Leu	Phe 360	Thr	Thr	Ala	Ile	Gln 365	Arg	Trp	Asp
Ile	Glu	Ser	Met	Lys	Gln	Leu	Pro	Pro	Tyr	Met	Gln	Ile	Cys	Tyr	Leu

370	375	380
Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr Leu Arg Asp 385 390 395 400		
Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp Val Asp Leu 405 410 415		
Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met Gly His Lys 420 425 430		
Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser Ile Gly Gly 435 440 445		
Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp Ser Ile Glu 450 455 460		
Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile Val Arg Ala 465 470 475 480		
Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp 485 490 495		
Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys Tyr Met Asn 500 505 510		
Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val Arg Ser Leu 515 520 525		
Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met Thr Ser Ser 530 535 540		
Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala Arg Met Ala 545 550 555 560		
Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met Gln His Ser 565 570 575		
Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg Tyr Glu 580 585 590		

<210> 72

<211> 1967

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
computer-generated nucleic acid sequence

<220>

<221> CDS

<222> (13)..(1785)

<223> computer-generated nucleic acid sequence encoding
1,8 cineole synthase

<400> 72

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gcc aaa att ttt cac aat aac tta ttc agc gtg att tca aaa cga cat				99
Ala Lys Ile Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His				
15 20 25				
cgt ttc agt act aca atc acc act cgt ggt ggc agg tgg gca cat tgc				147
Arg Phe Ser Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys				
30 35 40 45				
tca cta caa atg ggt aat gag atc caa act gga cga cga act gga ggc				195
Ser Leu Gln Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly				
50 55 60				
tac cag cct acc ctt tgg gat ttc agc acc ctt caa ttg ttc gac tct				243
Tyr Gln Pro Thr Leu Trp Asp Phe Ser Thr Leu Gln Leu Phe Asp Ser				
65 70 75				
gag tat aag gaa gag aag cac ttg atg agg gcc gca ggt atg ata gcc				291
Glu Tyr Lys Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala				
80 85 90				
caa gtg aat atg ttg ttg cag gaa gaa gta gat tcg att caa cgg ttg				339
Gln Val Asn Met Leu Leu Gln Glu Glu Val Asp Ser Ile Gln Arg Leu				
95 100 105				
gag ttg att gat gac cta cga agg ctg ggt ata tct tgc cat ttt gac				387
Glu Leu Ile Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp				
110 115 120 125				
cgc gag atc gtt gaa ata tta aac tca aaa tat tat acc aac aat gag				435
Arg Glu Ile Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu				
130 135 140				
ata gat gaa agt gat cta tac tca aca gcc ctt aga ttc aag ctc cta				483
Ile Asp Glu Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu				
145 150 155				
aga caa tac gat ttt agc gtc tct caa gag gta ttt gat tgt ttc aag				531
Arg Gln Tyr Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys				
160 165 170				
aat gac aag ggt act gat ttc aag cca agc cta gtc gat gat act aga				579
Asn Asp Lys Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg				
175 180 185				
gga ttg tta caa ttg tac gaa gct tcg ttt tta tca gca caa ggc gaa				627
Gly Leu Leu Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu				
190 195 200 205				
gaa acc cta cat ctt gcc aga gat ttt gct act aaa ttt ctg cat aaa				675
Glu Thr Leu His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys				
210 215 220				
aga gta cta gtt gat aaa gac att aat ctc tta tca tca att gaa cgt				723
Arg Val Leu Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg				
225 230 235				
gcg ttg gag ttg cct act cat tgg agg gtt caa atg ccc aac gca aga				771
Ala Leu Glu Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg				

240	245	250	
tcc ttc att gat gct tat aag agg aga ccc gac atg aat ccg act gtg Ser Phe Ile Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val 255 260 265			819
cta gaa cta gct aaa ttg gac ttc aat atg gtt caa gca caa ttt caa Leu Glu Leu Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln 270 275 280 285			867
caa gag ctc aaa gag gcc tct agg tgg tgg aat agt acg ggt ctt gtc Gln Glu Leu Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val 290 295 300			915
cac gag ctt ccc ttt gtg aga gat agg att gtg gaa tgc tac tac tgg His Glu Leu Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp 305 310 315			963
acg aca gga gtg gtt gag cgt cgt gaa cat gga tac gag agg ata atg Thr Thr Gly Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met 320 325 330			1011
ctc acc aaa ata aat gct ctt gtt aca aca ata gac gat gtc ttt gat Leu Thr Lys Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp 335 340 345			1059
att tat ggt acg ctt gaa gag cta caa cta ttc aca act gct att caa Ile Tyr Gly Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln 350 355 360 365			1107
aga tgg gat att gaa tca atg aag caa ctc cct cct tac atg caa ata Arg Trp Asp Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile 370 375 380			1155
tgt tat ctt gct ctc ttc aac ttt gtg aat gag atg gct tat gat act Cys Tyr Leu Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr 385 390 395			1203
ctt agg gat aaa ggt ttc aac tcc acc cca tat cta cga aaa gcg tgg Leu Arg Asp Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp 400 405 410			1251
gtt gat ttg gtt gag tca tat cta ata gag gca aag tgg tac tac atg Val Asp Leu Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met 415 420 425			1299
gga cat aaa cct agt ttg gaa gaa tat atg aag aat agt tgg ata tca Gly His Lys Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser 430 435 440 445			1347
atc gga ggc atc ccc att cta tct cat cta ttt ttc cgg cta aca gat Ile Gly Gly Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp 450 455 460			1395
tcg att gag gaa gag gat gct gag agt atg cat aaa tac cat gat att Ser Ile Glu Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile 465 470 475			1443
gtt cgt gca tcg tgt act att cta agg ctt gct gat gat atg gga aca Val Arg Ala Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr			1491

480	485	490	
tcg ctg gat gag gtg gag aga ggc gac gtg ccc aaa tca gtt cag tgc			1539
Ser Leu Asp Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys			
495	500	505	
tac atg aat gag aag aat gct tcg gaa gaa gaa gcg cga gag cat gtg			1587
Tyr Met Asn Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val			
510	515	520	525
cga tca ctc ata gac caa aca tgg aag atg atg aac aag gaa atg atg			1635
Arg Ser Leu Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met			
	530	535	540
acg tca tca ttt tcc aaa tat ttt gta caa gtt tct gct aat ctt gca			1683
Thr Ser Ser Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala			
	545	550	555
aga atg gcg caa tgg ata tac cag cat gaa tct gat gga ttt ggc atg			1731
Arg Met Ala Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met			
	560	565	570
caa cat tca ttg gtg aac aaa atg ctc aga ggg ttg ttg ttc gac cgc			1779
Gln His Ser Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg			
	575	580	585
tat gag taactaatct tcgcccgggt tccaaatgaa tcaatctgtt gtgttgctgt			1935
Tyr Glu			
590			
tccacctgat atcaataata attagacaaa tgtttctgta cgggtggccc aaccgtcagg			1895
cccatcttcgc tcatgttcat aataaataat aaaactgtta atcaataaca aaaaaaaaaa			1955
aaaaaaaaaa aa			1967

<210> 73

<211> 591

<212> PRT

<213> Artificial Sequence

<400> 73

Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro Ala Lys Ile	
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Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His Arg Phe Ser	
20	30
Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys Ser Leu Gln	
35	45
Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro	
50	60
Thr Leu Trp Asp Phe Ser Thr Leu Gln Leu Phe Asp Ser Glu Tyr Lys	
65	80
Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala Gln Val Asn	
85	95

Met Leu Leu Gln Glu Glu Val Asp Ser Ile Gln Arg Leu Glu Leu Ile
 100 105 110
 Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp Arg Glu Ile
 115 120 125
 Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu Ile Asp Glu
 130 135 140
 Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr
 145 150 155 160
 Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys
 165 170 175
 Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg Gly Leu Leu
 180 185 190
 Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu Glu Thr Leu
 195 200 205
 His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys Arg Val Leu
 210 215 220
 Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg Ala Leu Glu
 225 230 235 240
 Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg Ser Phe Ile
 245 250 255
 Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val Leu Glu Leu
 260 265 270
 Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln Gln Glu Leu
 275 280 285
 Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val His Glu Leu
 290 295 300
 Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp Thr Thr Gly
 305 310 315 320
 Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met Leu Thr Lys
 325 330 335
 Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp Ile Tyr Gly
 340 345 350
 Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln Arg Trp Asp
 355 360 365
 Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile Cys Tyr Leu
 370 375 380
 Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr Leu Arg Asp
 385 390 395 400
 Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp Val Asp Leu
 405 410 415

Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met Gly His Lys
420 425 430

Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser Ile Gly Gly
435 440 445

Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp Ser Ile Glu
450 455 460

Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile Val Arg Ala
465 470 475 480

Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp
485 490 495

Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys Tyr Met Asn
500 505 510

Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val Arg Ser Leu
515 520 525

Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met Thr Ser Ser
530 535 540

Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala Arg Met Ala
545 550 555 560

Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met Gln His Ser
565 570 575

Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg Tyr Glu
580 585 590

<210> 74

<211> 1967

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
computer-generated nucleic acid sequence

<220>

<221> CDS

<222> (13)..(1785)

<223> computer-generated nucleic acid sequence encoding
1,8 cineole synthase

<400> 74

gacaccaca ag atg tcg agt ctt ata atg caa gtt gtt att cct aag cca 51
Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro
1 5 10

gcc aaa att ttt cac aat aac tta ttc agc gtg att tca aaa cga cat 99
Ala Lys Ile Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His
15 20 25

cgt ttc agt act aca atc acc act cgt ggt ggc agg tgg gca cat tgc 147

Arg	Phe	Ser	Thr	Thr	Ile	Thr	Thr	Arg	Gly	Gly	Arg	Trp	Ala	His	Cys	
30					35				40						45	
tca	cta	caa	atg	ggt	aat	gag	atc	caa	act	gga	cga	cga	act	gga	ggc	195
Ser	Leu	Gln	Met	Gly	Asn	Glu	Ile	Gln	Thr	Gly	Arg	Arg	Thr	Gly	Gly	
				50				55						60		
tac	cag	cct	acc	ctt	tgg	gat	ttc	agc	acc	att	caa	gtg	ttc	gac	tct	243
Tyr	Gln	Pro	Thr	Leu	Trp	Asp	Phe	Ser	Thr	Ile	Gln	Val	Phe	Asp	Ser	
			65					70					75			
gag	tat	aag	gaa	gag	aag	cac	ttg	atg	agg	gcc	gca	ggt	atg	ata	gcc	291
Glu	Tyr	Lys	Glu	Glu	Lys	His	Leu	Met	Arg	Ala	Ala	Gly	Met	Ile	Ala	
		80					85					90				
caa	gtg	aat	atg	ttg	ttg	cag	gaa	gaa	gta	gat	tcg	att	caa	cgg	ttg	339
Gln	Val	Asn	Met	Leu	Leu	Gln	Glu	Glu	Val	Asp	Ser	Ile	Gln	Arg	Leu	
	95					100				105						
gag	ttg	att	gat	gac	cta	cga	agg	ctg	ggt	ata	tct	tgc	cat	ttt	gac	387
Glu	Leu	Ile	Asp	Asp	Leu	Arg	Arg	Leu	Gly	Ile	Ser	Cys	His	Phe	Asp	
110					115				120						125	
cgc	gag	atc	ggt	gaa	ata	tta	aac	tca	aaa	tat	tat	acc	aac	aat	gag	435
Arg	Glu	Ile	Val	Glu	Ile	Leu	Asn	Ser	Lys	Tyr	Tyr	Thr	Asn	Asn	Glu	
				130					135					140		
ata	gat	gaa	agt	gat	cta	tac	tca	aca	gcc	ctt	aga	ttc	aag	ctc	cta	483
Ile	Asp	Glu	Ser	Asp	Leu	Tyr	Ser	Thr	Ala	Leu	Arg	Phe	Lys	Leu	Leu	
			145					150					155			
aga	caa	tac	gat	ttt	agc	gtc	tct	caa	gag	gta	ttt	gat	tgt	ttc	aag	531
Arg	Gln	Tyr	Asp	Phe	Ser	Val	Ser	Gln	Glu	Val	Phe	Asp	Cys	Phe	Lys	
		160					165					170				
aat	gac	aag	ggt	act	gat	ttc	aag	cca	agc	cta	gtc	gat	gat	act	aga	579
Asn	Asp	Lys	Gly	Thr	Asp	Phe	Lys	Pro	Ser	Leu	Val	Asp	Asp	Thr	Arg	
	175					180					185					
gga	ttg	tta	caa	ttg	tac	gaa	gct	tcg	ttt	tta	tca	gca	caa	ggc	gaa	627
Gly	Leu	Leu	Gln	Leu	Tyr	Glu	Ala	Ser	Phe	Leu	Ser	Ala	Gln	Gly	Glu	
190					195				200					205		
gaa	acc	cta	cat	ctt	gcc	aga	gat	ttt	gct	act	aaa	ttt	ctg	cat	aaa	675
Glu	Thr	Leu	His	Leu	Ala	Arg	Asp	Phe	Ala	Thr	Lys	Phe	Leu	His	Lys	
				210				215					220			
aga	gta	cta	ggt	gat	aaa	gac	att	aat	ctc	tta	tca	tca	att	gaa	cgt	723
Arg	Val	Leu	Val	Asp	Lys	Asp	Ile	Asn	Leu	Leu	Ser	Ser	Ile	Glu	Arg	
			225				230						235			
gcg	ttg	gag	ttg	cct	act	cat	tgg	agg	ggt	caa	atg	ccc	aac	gca	aga	771
Ala	Leu	Glu	Leu	Pro	Thr	His	Trp	Arg	Val	Gln	Met	Pro	Asn	Ala	Arg	
		240					245					250				
tcc	ttc	att	gat	gct	tat	aag	agg	aga	ccc	gac	atg	aat	ccg	act	gtg	819
Ser	Phe	Ile	Asp	Ala	Tyr	Lys	Arg	Arg	Pro	Asp	Met	Asn	Pro	Thr	Val	
	255					260					265					
cta	gaa	cta	gct	aaa	ttg	gac	ttc	aat	atg	ggt	caa	gca	caa	ttt	caa	867

Leu Glu Leu Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln 270 275 280 285	
caa gag ctc aaa gag gcc tct agg tgg tgg aat agt acg ggt ctt gtc Gln Glu Leu Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val 290 295 300	915
cac gag ctt ccc ttt gtg aga gat agg att gtg gaa tgc tac tac tgg His Glu Leu Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp 305 310 315	963
acg aca gga gtg gtt gag cgt cgt gaa cat gga tac gag agg ata atg Thr Thr Gly Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met 320 325 330	1011
ctc acc aaa ata aat gct ctt gtt aca aca ata gac gat gtc ttt gat Leu Thr Lys Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp 335 340 345	1059
att tat ggt acg ctt gaa gag cta caa cta ttc aca act gct att caa Ile Tyr Gly Thr Leu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln 350 355 360 365	1107
aga tgg gat att gaa tca atg aag caa ctc cct cct tac atg caa ata Arg Trp Asp Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile 370 375 380	1155
tgt tat ctt gct ctc ttc aac ttt gtg aat gag atg gct tat gat act Cys Tyr Leu Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr 385 390 395	1203
ctt agg gat aaa ggt ttc aac tcc acc cca tat cta cga aaa gcg tgg Leu Arg Asp Lys Gly Phe Asn Thr Pro Tyr Leu Arg Lys Ala Trp 400 405 410	1251
gtt gat ttg gtt gag tca tat cta ata gag gca aag tgg tac tac atg Val Asp Leu Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met 415 420 425	1299
gga cat aaa cct agt ttg gaa gaa tat atg aag aat agt tgg ata tca Gly His Lys Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser 430 435 440 445	1347
atc gga ggc atc ccc att cta tct cat cta ttt ttc cgg cta aca gat Ile Gly Gly Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp 450 455 460	1395
tcg att gag gaa gag gat gct gag agt atg cat aaa tac cat gat att Ser Ile Glu Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile 465 470 475	1443
gtt cgt gca tcg tgt act att cta agg ctt gct gat gat atg gga aca Val Arg Ala Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr 480 485 490	1491
tcg ctg gat gag gtg gag aga ggc gac gtg ccc aaa tca gtt cag tgc Ser Leu Asp Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys 495 500 505	1539
tac atg aat gag aag aat gct tcg gaa gaa gaa gcg cga gag cat gtg	1587

Tyr Met Asn Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val
 510 515 520 525
 cga tca ctc ata gac caa aca tgg aag atg atg aac aag gaa atg atg 1635
 Arg Ser Leu Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met 540
 530 535
 acg tca tca ttt tcc aaa tat ttt gta caa gtt tct gct aat ctt gca 1683
 Thr Ser Ser Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala 555
 545 550
 aga atg gcg caa tgg ata tac cag cat gaa tct gat gga ttt ggc atg 1731
 Arg Met Ala Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met 570
 560 565
 caa cat tca ttg gtg aac aaa atg ctc aga ggg ttg ttg ttc gac cgc 1779
 Gln His Ser Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg 585
 575 580
 tat gag taactaatct tcgcccgggt tccaaatgaa tcaatctgtt gtgttgctgt 1835
 Tyr Glu 590
 tccacctgat atcaataata attagacaaa tgtttctgta cgggtggccc aaccgtcagg 1895
 cccatttcgc tcatgttcat aataaataat aaaactgtta atcaataaca aaaaaaaaaa 1955
 aaaaaaaaaa aa 1967

<210> 75
 <211> 591
 <212> PRT
 <213> Artificial Sequence

<400> 75
 Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro Ala Lys Ile
 1 5 10 15
 Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His Arg Phe Ser
 20 25 30
 Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys Ser Leu Gln
 35 40 45
 Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro
 50 55 60
 Thr Leu Trp Asp Phe Ser Thr Ile Gln Val Phe Asp Ser Glu Tyr Lys
 65 70 75 80
 Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala Gln Val Asn
 85 90 95
 Met Leu Leu Gln Glu Glu Val Asp Ser Ile Gln Arg Leu Glu Leu Ile
 100 105 110
 Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp Arg Glu Ile
 115 120 125

Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu Ile Asp Glu
 130 135 140
 Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr
 145 150 155 160
 Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys
 165 170 175
 Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg Gly Leu Leu
 180 185 190
 Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu Glu Thr Leu
 195 200 205
 His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys Arg Val Leu
 210 215 220
 Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg Ala Leu Glu
 225 230 235 240
 Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg Ser Phe Ile
 245 250 255
 Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val Leu Glu Leu
 260 265 270
 Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln Gln Glu Leu
 275 280 285
 Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val His Glu Leu
 290 295 300
 Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp Thr Thr Gly
 305 310 315 320
 Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met Leu Thr Lys
 325 330 335
 Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp Ile Tyr Gly
 340 345 350
 Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln Arg Trp Asp
 355 360 365
 Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile Cys Tyr Leu
 370 375 380
 Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr Leu Arg Asp
 385 390 395 400
 Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp Val Asp Leu
 405 410 415
 Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met Gly His Lys
 420 425 430
 Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser Ile Gly Gly
 435 440 445

Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp Ser Ile Glu
 450 455 460
 Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile Val Arg Ala
 465 470 475 480
 Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp
 485 490 495
 Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys Tyr Met Asn
 500 505 510
 Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val Arg Ser Leu
 515 520 525
 Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met Thr Ser Ser
 530 535 540
 Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala Arg Met Ala
 545 550 555 560
 Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met Gln His Ser
 565 570 575
 Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg Tyr Glu
 580 585 590

<210> 76

<211> 1967

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 computer-generated nucleic acid sequence

<220>

<221> CDS

<222> (13)..(1785)

<223> computer-generated nucleic acid sequence encoding
 1,8 cineole synthase

<400> 76

gatcaccaca ag atg tcg agt ctt ata atg caa gtt gtt att cct aag cca 51
 Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro
 1 5 10

gcc aaa att ttt cac aat aac tta ttc agc gtg att tca aaa cga cat 99
 Ala Lys Ile Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His
 15 20 25

cgt ttc agt act aca atc acc act cgt ggt ggc agg tgg gca cat tgc 147
 Arg Phe Ser Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys
 30 35 40 45

tca cta caa atg ggt aat gag atc caa act gga cga cga act gga ggc 195
 Ser Leu Gln Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly
 50 55 60

tac cag cct acc ctt tgg gat ttc agc acc att caa ttg ttc gac tct Tyr Gln Pro Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser 65 70 75	243
gag tat aag gaa gag aag cac gtg atg agg gcc gca ggt atg ata gcc Glu Tyr Lys Glu Glu Lys His Val Met Arg Ala Ala Gly Met Ile Ala 80 85 90	291
caa gtg aat atg ttg ttg cag gaa gaa gta gat tcg att caa cgg ttg Gln Val Asn Met Leu Leu Gln Glu Glu Val Asp Ser Ile Gln Arg Leu 95 100 105	339
gag ttg att gat gac cta cga agg ctg ggt ata tct tgc cat ttt gac Glu Leu Ile Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp 110 115 120 125	387
cgc gag atc gtt gaa ata tta aac tca aaa tat tat acc aac aat gag Arg Glu Ile Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu 130 135 140	435
ata gat gaa agt gat cta tac tca aca gcc ctt aga ttc aag ctc cta Ile Asp Glu Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu 145 150 155	483
aga caa tac gat ttt agc gtc tct caa gag gta ttt gat tgt ttc aag Arg Gln Tyr Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys 160 165 170	531
aat gac aag ggt act gat ttc aag cca agc cta gtc gat gat act aga Asn Asp Lys Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg 175 180 185	579
gga ttg tta caa ttg tac gaa gct tcg ttt tta tca gca caa ggc gaa Gly Leu Leu Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu 190 195 200 205	627
gaa acc cta cat ctt gcc aga gat ttt gct act aaa ttt ctg cat aaa Glu Thr Leu His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys 210 215 220	675
aga gta cta gtt gat aaa gac att aat ctc tta tca tca att gaa cgt Arg Val Leu Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg 225 230 235	723
gcg ttg gag ttg cct act cat tgg agg gtt caa atg ccc aac gca aga Ala Leu Glu Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg 240 245 250	771
tcc ttc att gat gct tat aag agg aga ccc gac atg aat ccg act gtg Ser Phe Ile Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val 255 260 265	819
cta gaa cta gct aaa ttg gac ttc aat atg gtt caa gca caa ttt caa Leu Glu Leu Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln 270 275 280 285	867
caa gag ctc aaa gag gcc tct agg tgg tgg aat agt acg ggt ctt gtc Gln Glu Leu Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val 290 295 300	915

cac gag ctt ccc ttt gtg aga gat agg att gtg gaa tgc tac tac tgg	963
His Glu Leu Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp	
305 310 315	
acg aca gga gtg gtt gag cgt cgt gaa cat gga tac gag agg ata atg	1011
Thr Thr Gly Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met	
320 325 330	
ctc acc aaa ata aat gct ctt gtt aca aca ata gac gat gtc ttt gat	1059
Leu Thr Lys Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp	
335 340 345	
att tat ggt acg ctt gaa gag cta caa cta ttc aca act gct att caa	1107
Ile Tyr Gly Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln	
350 355 360 365	
aga tgg gat att gaa tca atg aag caa ctc cct cct tac atg caa ata	1155
Arg Trp Asp Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile	
370 375 380	
tgt tat ctt gct ctc ttc aac ttt gtg aat gag atg gct tat gat act	1203
Cys Tyr Leu Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr	
385 390 395	
ctt agg gat aaa ggt ttc aac tcc acc cca tat cta cga aaa gcg tgg	1251
Leu Arg Asp Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp	
400 405 410	
gtt gat ttg gtt gag tca tat cta ata gag gca aag tgg tac tac atg	1299
Val Asp Leu Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met	
415 420 425	
gga cat aaa cct agt ttg gaa gaa tat atg aag aat agt tgg ata tca	1347
Gly His Lys Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser	
430 435 440 445	
atc gga ggc atc ccc att cta tct cat cta ttt ttc cgg cta aca gat	1395
Ile Gly Gly Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp	
450 455 460	
tcg att gag gaa gag gat gct gag agt atg cat aaa tac cat gat att	1443
Ser Ile Glu Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile	
465 470 475	
gtt cgt gca tcg tgt act att cta agg ctt gct gat gat atg gga aca	1491
Val Arg Ala Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr	
480 485 490	
tcg ctg gat gag gtg gag aga ggc gac gtg ccc aaa tca gtt cag tgc	1539
Ser Leu Asp Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys	
495 500 505	
tac atg aat gag aag aat gct tcg gaa gaa gaa gcg cga gag cat gtg	1587
Tyr Met Asn Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val	
510 515 520 525	
cga tca ctc ata gac caa aca tgg aag atg atg aac aag gaa atg atg	1635
Arg Ser Leu Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met	
530 535 540	

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acg tca tca ttt tcc aaa tat ttt gta caa gtt tct gct aat ctt gca 1683
Thr Ser Ser Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala
          545          550          555

aga atg gcg caa tgg ata tac cag cat gaa tct gat gga ttt ggc atg 1731
Arg Met Ala Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met
          560          565          570

caa cat tca ttg gtg aac aaa atg ctc aga ggg ttg ttg ttc gac cgc 1779
Gln His Ser Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg
          575          580          585

tat gag taactaatct tcgcccgggt tccaaatgaa tcaatctgtt gtgttgctgt 1835
Tyr Glu
590

tccacctgat atcaataata attagacaaa tgtttctgta cgggtggccc aaccgtcagg 1895

cccatttcgc tcatgttcat aataaataat aaaactgtta atcaataaca aaaaaaaaaa 1955

aaaaaaaaaa aa 1967

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<210> 77
 <211> 591
 <212> PRT
 <213> Artificial Sequence

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<400> 77
Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro Ala Lys Ile
  1              5              10              15

Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His Arg Phe Ser
          20              25              30

Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys Ser Leu Gln
          35              40              45

Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro
          50              55              60

Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser Glu Tyr Lys
          65              70              75              80

Glu Glu Lys His Val Met Arg Ala Ala Gly Met Ile Ala Gln Val Asn
          85              90              95

Met Leu Leu Gln Glu Glu Val Asp Ser Ile Gln Arg Leu Glu Leu Ile
          100              105              110

Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp Arg Glu Ile
          115              120              125

Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu Ile Asp Glu
          130              135              140

Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr
          145              150              155              160

Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys

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485										490					495						
Glu	Val	Glu	Arg	Gly	Asp	Val	Pro	Lys	Ser	Val	Gln	Cys	Tyr	Met	Asn						
			500					505					510								
Glu	Lys	Asn	Ala	Ser	Glu	Glu	Glu	Ala	Arg	Glu	His	Val	Arg	Ser	Leu						
		515					520					525									
Ile	Asp	Gln	Thr	Trp	Lys	Met	Met	Asn	Lys	Glu	Met	Met	Thr	Ser	Ser						
	530					535					540										
Phe	Ser	Lys	Tyr	Phe	Val	Gln	Val	Ser	Ala	Asn	Leu	Ala	Arg	Met	Ala						
545					550					555					560						
Gln	Trp	Ile	Tyr	Gln	His	Glu	Ser	Asp	Gly	Phe	Gly	Met	Gln	His	Ser						
				565					570					575							
Leu	Val	Asn	Lys	Met	Leu	Arg	Gly	Leu	Leu	Phe	Asp	Arg	Tyr	Glu							
		580						585					590								

<210> 78

<211> 1967

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
computer-generated nucleic acid sequence

<220>

<221> CDS

<222> (13)..(1785)

<223> computer-generated nucleic acid sequence encoding
1,8 cineole synthase

<400> 78

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gatcaccaca ag atg tcg agt ctt ata atg caa gtt gtt att cct aag cca 51
      Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro
        1                      5                      10

gcc aaa att ttt cac aat aac tta ttc agc gtg att tca aaa cga cat 99
Ala Lys Ile Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His
  15                      20                      25

cgt ttc agt act aca atc acc act cgt ggt ggc agg tgg gca cat tgc 147
Arg Phe Ser Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys
  30                      35                      40                      45

tca cta caa atg ggt aat gag atc caa act gga cga cga act gga ggc 195
Ser Leu Gln Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly
      50                      55                      60

tac cag cct acc ctt tgg gat ttc agc acc att caa ttg ttc gac tct 243
Tyr Gln Pro Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser
      65                      70                      75

gag tat aag gaa gag aag cac ttg atg agg gcc gca ggt atg cta gcc 291
Glu Tyr Lys Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Leu Ala
  80                      85                      90

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caa gtg aat atg ttg ttg cag gaa gaa gta gat tcg att caa cgg ttg	339
Gln Val Asn Met Leu Leu Gln Glu Glu Val Asp Ser Ile Gln Arg Leu	
95 100 105	
gag ttg att gat gac cta cga agg ctg ggt ata tct tgc cat ttt gac	387
Glu Leu Ile Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp	
110 115 120 125	
cgc gag atc gtt gaa ata tta aac tca aaa tat tat acc aac aat gag	435
Arg Glu Ile Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu	
130 135 140	
ata gat gaa agt gat cta tac tca aca gcc ctt aga ttc aag ctc cta	483
Ile Asp Glu Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu	
145 150 155	
aga caa tac gat ttt agc gtc tct caa gag gta ttt gat tgt ttc aag	531
Arg Gln Tyr Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys	
160 165 170	
aat gac aag ggt act gat ttc aag cca agc cta gtc gat gat act aga	579
Asn Asp Lys Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg	
175 180 185	
gga ttg tta caa ttg tac gaa gct tcg ttt tta tca gca caa ggc gaa	627
Gly Leu Leu Gln Leu Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu	
190 195 200 205	
gaa acc cta cat ctt gcc aga gat ttt gct act aaa ttt ctg cat aaa	675
Glu Thr Leu His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys	
210 215 220	
aga gta cta gtt gat aaa gac att aat ctc tta tca tca att gaa cgt	723
Arg Val Leu Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg	
225 230 235	
gcg ttg gag ttg cct act cat tgg agg gtt caa atg ccc aac gca aga	771
Ala Leu Glu Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg	
240 245 250	
tcc ttc att gat gct tat aag agg aga ccc gac atg aat ccg act gtg	819
Ser Phe Ile Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val	
255 260 265	
cta gaa cta gct aaa ttg gac ttc aat atg gtt caa gca caa ttt caa	867
Leu Glu Leu Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln	
270 275 280 285	
caa gag ctc aaa gag gcc tct agg tgg tgg aat agt acg ggt ctt gtc	915
Gln Glu Leu Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val	
290 295 300	
cac gag ctt ccc ttt gtg aga gat agg att gtg gaa tgc tac tac tgg	963
His Glu Leu Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp	
305 310 315	
acg aca gga gtg gtt gag cgt cgt gaa cat gga tac gag agg ata atg	1011
Thr Thr Gly Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met	
320 325 330	

ctc acc aaa ata aat gct ctt gtt aca aca ata gac gat gtc ttt gat Leu Thr Lys Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp 335 340 345	1059
att tat ggt acg ctt gaa gag cta caa cta ttc aca act gct att caa Ile Tyr Gly Thr Leu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln 350 355 360 365	1107
aga tgg gat att gaa tca atg aag caa ctc cct cct tac atg caa ata Arg Trp Asp Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile 370 375 380	1155
tgt tat ctt gct ctc ttc aac ttt gtg aat gag atg gct tat gat act Cys Tyr Leu Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr 385 390 395	1203
ctt agg gat aaa ggt ttc aac tcc acc cca tat cta cga aaa gcg tgg Leu Arg Asp Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp 400 405 410	1251
gtt gat ttg gtt gag tca tat cta ata gag gca aag tgg tac tac atg Val Asp Leu Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met 415 420 425	1299
gga cat aaa cct agt ttg gaa gaa tat atg aag aat agt tgg ata tca Gly His Lys Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser 430 435 440 445	1347
atc gga ggc atc ccc att cta tct cat cta ttt ttc cgg cta aca gat Ile Gly Gly Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp 450 455 460	1395
tcg att gag gaa gag gat gct gag agt atg cat aaa tac cat gat att Ser Ile Glu Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile 465 470 475	1443
gtt cgt gca tcg tgt act att cta agg ctt gct gat gat atg gga aca Val Arg Ala Ser Cys Thr Ile Leu Arg Leu Ala Asp Met Gly Thr 480 485 490	1491
tcg ctg gat gag gtg gag aga ggc gac gtg ccc aaa tca gtt cag tgc Ser Leu Asp Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys 495 500 505	1539
tac atg aat gag aag aat gct tcg gaa gaa gaa gcg cga gag cat gtg Tyr Met Asn Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val 510 515 520 525	1587
cga tca ctc ata gac caa aca tgg aag atg atg aac aag gaa atg atg Arg Ser Leu Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met 530 535 540	1635
acg tca tca ttt tcc aaa tat ttt gta caa gtt tct gct aat ctt gca Thr Ser Ser Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala 545 550 555	1683
aga atg gcg caa tgg ata tac cag cat gaa tct gat gga ttt ggc atg Arg Met Ala Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met 560 565 570	1731

caa cat tca ttg gtg aac aaa atg ctg aga ggg ttg ttg ttc gac cgc 1779
 Gln His Ser Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg
 575 580 585

tac gag taactaatct tcgcccgggt tccaaatgaa tcaatctgtt gtgttgctgt 1835
 Tyr Glu
 590

tccacctgat atcaataata attagacaaa tgtttctgta cgggtggccc aaccgtcagg 1895

cccatttcgc tcattgttcac aataaataat aaaactgtta atcaataaca aaaaaaaaaa 1955

aaaaaaaaaa aa 1967

<210> 79

<211> 591

<212> PRT

<213> Artificial Sequence

<400> 79

Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro Ala Lys Ile
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Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His Arg Phe Ser
 20 25 30

Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys Ser Leu Gln
 35 40 45

Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro
 50 55 60

Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser Glu Tyr Lys
 65 70 75 80

Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Leu Ala Gln Val Asn
 85 90 95

Met Leu Leu Gln Glu Glu Val Asp Ser Ile Gln Arg Leu Glu Leu Ile
 100 105 110

Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp Arg Glu Ile
 115 120 125

Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu Ile Asp Glu
 130 135 140

Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr
 145 150 155 160

Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys
 165 170 175

Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg Gly Leu Leu
 180 185 190

Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu Glu Thr Leu
 195 200 205

His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys Arg Val Leu
 210 215 220
 Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg Ala Leu Glu
 225 230 235 240
 Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg Ser Phe Ile
 245 250 255
 Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val Leu Glu Leu
 260 265 270
 Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln Gln Glu Leu
 275 280 285
 Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val His Glu Leu
 290 295 300
 Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp Thr Thr Gly
 305 310 315 320
 Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met Leu Thr Lys
 325 330 335
 Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp Ile Tyr Gly
 340 345 350
 Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln Arg Trp Asp
 355 360 365
 Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile Cys Tyr Leu
 370 375 380
 Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr Leu Arg Asp
 385 390 395 400
 Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp Val Asp Leu
 405 410 415
 Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met Gly His Lys
 420 425 430
 Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser Ile Gly Gly
 435 440 445
 Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp Ser Ile Glu
 450 455 460
 Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile Val Arg Ala
 465 470 475 480
 Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp
 485 490 495
 Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys Tyr Met Asn
 500 505 510
 Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val Arg Ser Leu
 515 520 525

Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met Thr Ser Ser
 530 535 540

Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala Arg Met Ala
 545 550 555 560

Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met Gln His Ser
 565 570 575

Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg Tyr Glu
 580 585 590

<210> 80

<211> 1967

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 computer-generated nucleic acid sequence

<220>

<221> CDS

<222> (13)..(1785)

<223> computer-generated nucleic acid sequence encoding
 1,8 cineole synthase

<400> 80

gatcaccaca ag atg tcg agt ctt ata atg caa gtt gtt att cct aag cca 51
 Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro
 1 5 10

gcc aaa att ttt cac aat aac tta ttc agc gtg att tca aaa cga cat 99
 Ala Lys Ile Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His
 15 20 25

cgt ttc agt act aca atc acc act cgt ggt ggc agg tgg gca cat tgc 147
 Arg Phe Ser Thr Thr Thr Arg Gly Gly Arg Trp Ala His Cys
 30 35 40 45

tca cta caa atg ggt aat gag atc caa act gga cga cga act gga ggc 195
 Ser Leu Gln Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly
 50 55 60

tac cag cct acc ctt tgg gat ttc agc acc att caa ttg ttc gac tct 243
 Tyr Gln Pro Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser
 65 70 75

gag tat aag gaa gag aag cac ttg atg agg gcc gca ggt atg ata gcc 291
 Glu Tyr Lys Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala
 80 85 90

caa ctg aat atg ttg ttg cag gaa gaa gta gat tcg att caa cgg ttg 339
 Gln Leu Asn Met Leu Leu Gln Glu Glu Val Asp Ser Ile Gln Arg Leu
 95 100 105

gag ttg att gat gac cta cga agg ctg ggt ata tct tgc cat ttt gac 387
 Glu Leu Ile Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp

110	115	120	125	
cgc gag atc gtt Arg Glu Ile Val	gaa ata tta aac tca Glu Ile Leu Asn Ser 130	aaa tat tat acc aac aat gag Lys Tyr Tyr Thr Asn Asn Glu 135 140	435	
ata gat gaa agt gat Ile Asp Glu Ser 145	cta tac tca aca gcc Leu Tyr Ser Thr Ala 150	ctt aga ttc aag ctc cta Leu Arg Phe Lys Leu Leu 155	483	
aga caa tac gat ttt Arg Gln Tyr Asp Phe 160	agc gtc tct caa gag Ser Val Ser Gln Glu 165	gta ttt gat tgt ttc aag Val Phe Asp Cys Phe Lys 170	531	
aat gac aag ggt act Asn Asp Lys Gly Thr 175	gat ttc aag cca agc Tyr Asp Phe Lys Pro 180	cta gtc gat gat act aga Leu Val Asp Asp Thr Arg 185	579	
gga ttg tta caa ttg Gly Leu Leu Gln Leu 190	tac gaa gct tcg ttt Glu Ala Ser Phe 195	tta tca gca caa ggc gaa Leu Ser Ala Gln Gly 200 205	627	
gaa acc cta cat ctt Glu Thr Leu His Leu 210	gcc aga gat ttt gct Ala Ala Arg Asp Phe 215	act aaa ttt ctg cat aaa Thr Lys Phe Leu His Lys 220	675	
aga gta cta gtt gat Arg Val Leu Val Asp 225	aaa gac att aat ctc Lys Asp Ile Asn Leu 230	tta tca tca att gaa cgt Leu Leu Ser Ser Ile Glu Arg 235	723	
gcg ttg gag ttg cct Ala Leu Glu Leu Pro 240	act cat tgg agg gtt Thr His Trp Arg Val 245	caa atg ccc aac gca aga Gln Met Pro Asn Ala Arg 250	771	
tcc ttc att gat gct Ser Phe Ile Asp Ala 255	tat aag agg aga ccc Tyr Lys Arg Arg Pro 260	gac atg aat ccg act gtg Asp Met Asn Pro Thr Val 265	819	
cta gaa cta gct aaa Leu Glu Leu Ala Lys 270	ttg gac ttc aat atg Leu Asp Phe Asn Met 275 280	ggt caa gca caa ttt caa Val Gln Ala Gln Phe Gln 285	867	
caa gag ctc aaa gag Gln Glu Leu Lys Glu 290	gcc tct agg tgg tgg Ala Ser Arg Trp Trp 295	aat agt acg ggt ctt gtc Asn Ser Thr Gly Leu Val 300	915	
cac gag ctt ccc ttt His Glu Leu Pro Phe 305	gtg aga gat agg att Val Arg Asp Arg Ile 310	gtg gaa tgc tac tac tgg Val Glu Cys Tyr Tyr Trp 315	963	
acg aca gga gtg gtt Thr Thr Gly Val Val 320	gag cgt cgt gaa cat Glu Arg Arg Glu His 325	gga tac gag agg ata atg Gly Tyr Glu Arg Ile Met 330	1011	
ctc acc aaa ata aat Leu Thr Lys Ile Asn 335	gct ctt gtt aca aca Ala Leu Val Thr Thr 340	ata gac gat gtc ttt gat Ile Asp Asp Val Phe Asp 345	1059	
att tat ggt acg ctt Ile Tyr Gly Thr Leu 350	gaa gag cta caa cta Glu Glu Leu Gln Leu 355	ttc aca act gct att caa Phe Thr Thr Ala Ile Gln 360	1107	

350	355	360	365	
aga tgg gat att gaa tca atg aag caa ctc cct cct tac atg caa ata Arg Trp Asp Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile 370 375 380				1155
tgt tat ctt gct ctc ttc aac ttt gtg aat gag atg gct tat gat act Cys Tyr Leu Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr 385 390 395				1203
ctt agg gat aaa ggt ttc aac tcc acc cca tat cta cga aaa gcg tgg Leu Arg Asp Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp 400 405 410				1251
gtt gat ttg gtt gag tca tat cta ata gag gca aag tgg tac tac atg Val Asp Leu Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met 415 420 425				1299
gga cat aaa cct agt ttg gaa gaa tat atg aag aat agt tgg ata tca Gly His Lys Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser 430 435 440 445				1347
atc gga ggc atc ccc att cta tct cat cta ttt ttc cgg cta aca gat Ile Gly Gly Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp 450 455 460				1395
tcg att gag gaa gag gat gct gag agt atg cat aaa tac cat gat att Ser Ile Glu Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile 465 470 475				1443
gtt cgt gca tcg tgt act att cta agg ctt gct gat gat atg gga aca Val Arg Ala Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr 480 485 490				1491
tcg ctg gat gag gtg gag aga ggc gac gtg ccc aaa tca gtt cag tgc Ser Leu Asp Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys 495 500 505				1539
tac atg aat gag aag aat gct tcg gaa gaa gaa gcg cga gag cat gtg Tyr Met Asn Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val 510 515 520 525				1587
cga tca ctc ata gac caa aca tgg aag atg atg aac aag gaa atg atg Arg Ser Leu Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met 530 535 540				1635
acg tca tca ttt tcc aaa tat ttt gta caa gtt tct gct aat ctt gca Thr Ser Ser Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala 545 550 555				1683
aga atg gcg caa tgg ata tac cag cat gaa tct gat gga ttt ggc atg Arg Met Ala Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met 560 565 570				1731
caa cat tca ttg gtg aac aaa atg ctc aga ggg ttg ttg ttc gac cgc Gln His Ser Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg 575 580 585				1779
tat gag taactaatct tcgcccgggt tccaaatgaa tcaatctgtt gtgttgctgt Tyr Glu				1835

590

tccacctgat atcaataata attagacaaa tgtttctgta cgggtggccc aaccgtcagg 1895
 cccatttcgc tcatgttcat aataaataat aaaactgtta atcaataaca aaaaaaaaaa 1955*
 aaaaaaaaaa aa 1967

<210> 81

<211> 591

<212> PRT

<213> Artificial Sequence

<400> 81

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		20						25					30		
Thr	Thr	Ile	Thr	Thr	Arg	Gly	Gly	Arg	Trp	Ala	His	Cys	Ser	Leu	Gln
		35					40					45			
Met	Gly	Asn	Glu	Ile	Gln	Thr	Gly	Arg	Arg	Thr	Gly	Gly	Tyr	Gln	Pro
	50					55					60				
Thr	Leu	Trp	Asp	Phe	Ser	Thr	Ile	Gln	Leu	Phe	Asp	Ser	Glu	Tyr	Lys
65					70					75					80
Glu	Glu	Lys	His	Leu	Met	Arg	Ala	Ala	Gly	Met	Ile	Ala	Gln	Leu	Asn
				85					90					95	
Met	Leu	Leu	Gln	Glu	Glu	Val	Asp	Ser	Ile	Gln	Arg	Leu	Glu	Leu	Ile
			100					105					110		
Asp	Asp	Leu	Arg	Arg	Leu	Gly	Ile	Ser	Cys	His	Phe	Asp	Arg	Glu	Ile
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Val	Glu	Ile	Leu	Asn	Ser	Lys	Tyr	Tyr	Thr	Asn	Asn	Glu	Ile	Asp	Glu
	130					135					140				
Ser	Asp	Leu	Tyr	Ser	Thr	Ala	Leu	Arg	Phe	Lys	Leu	Leu	Arg	Gln	Tyr
145					150					155					160
Asp	Phe	Ser	Val	Ser	Gln	Glu	Val	Phe	Asp	Cys	Phe	Lys	Asn	Asp	Lys
				165					170					175	
Gly	Thr	Asp	Phe	Lys	Pro	Ser	Leu	Val	Asp	Asp	Thr	Arg	Gly	Leu	Leu
			180					185					190		
Gln	Leu	Tyr	Glu	Ala	Ser	Phe	Leu	Ser	Ala	Gln	Gly	Glu	Glu	Thr	Leu
		195					200					205			
His	Leu	Ala	Arg	Asp	Phe	Ala	Thr	Lys	Phe	Leu	His	Lys	Arg	Val	Leu
	210					215					220				
Val	Asp	Lys	Asp	Ile	Asn	Leu	Leu	Ser	Ser	Ile	Glu	Arg	Ala	Leu	Glu
225					230					235					240

Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg Ser Phe Ile
 245 250 255
 Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val Leu Glu Leu
 260 265 270
 Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln Gln Glu Leu
 275 280 285
 Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val His Glu Leu
 290 295 300
 Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp Thr Thr Gly
 305 310 315 320
 Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met Leu Thr Lys
 325 330 335
 Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp Ile Tyr Gly
 340 345 350
 Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln Arg Trp Asp
 355 360 365
 Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile Cys Tyr Leu
 370 375 380
 Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr Leu Arg Asp
 385 390 395 400
 Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp Val Asp Leu
 405 410 415
 Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met Gly His Lys
 420 425 430
 Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser Ile Gly Gly
 435 440 445
 Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp Ser Ile Glu
 450 455 460
 Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile Val Arg Ala
 465 470 475 480
 Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp
 485 490 495
 Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys Tyr Met Asn
 500 505 510
 Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val Arg Ser Leu
 515 520 525
 Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met Thr Ser Ser
 530 535 540
 Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala Arg Met Ala
 545 550 555 560

Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met Gln His Ser
 565 570 575

Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg Tyr Glu
 580 585 590

<210> 82

<211> 1967

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 computer-generated nucleic acid sequence

<220>

<221> CDS

<222> (13) .. (1785)

<223> computer-generated nucleic acid sequence encoding
 1,8 cineole synthase

<400> 82

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gcc aaa att ttt cac aat aac tta ttc agc gtg att tca aaa cga cat 99
Ala Lys Ile Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His
      15                      20                      25

cgt ttc agt act aca atc acc act cgt ggt ggc agg tgg gca cat tgc 147
Arg Phe Ser Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys
      30                      35                      40                      45

tca cta caa atg ggt aat gag atc caa act gga cga cga act gga ggc 195
Ser Leu Gln Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly
          50                      55                      60

tac cag cct acc ctt tgg gat ttc agc acc att caa ttg ttc gac tct 243
Tyr Gln Pro Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser
          65                      70                      75

gag tat aag gaa gag aag cac ttg atg agg gcc gca ggt atg ata gcc 291
Glu Tyr Lys Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala
      80                      85                      90

caa gtg aat atg gtg ttg cag gaa gaa gta gat tcg att caa cgg ttg 339
Gln Val Asn Met Val Leu Gln Glu Glu Val Asp Ser Ile Gln Arg Leu
      95                      100                      105

gag ttg att gat gac cta cga agg ctg ggt ata tct tgc cat ttt gac 387
Glu Leu Ile Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp
     110                      115                      120                      125

cgc gag atc gtt gaa ata tta aac tca aaa tat tat acc aac aat gag 435
Arg Glu Ile Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu
          130                      135                      140

ata gat gaa agt gat cta tac tca aca gcc ctt aga ttc aag ctc cta 483

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Ile	Asp	Glu	Ser	Asp	Leu	Tyr	Ser	Thr	Ala	Leu	Arg	Phe	Lys	Leu	Leu		
			145					150					155				
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Arg	Gln	Tyr	Asp	Phe	Ser	Val	Ser	Gln	Glu	Val	Phe	Asp	Cys	Phe	Lys		
		160					165					170					
aat	gac	aag	ggg	act	gat	ttc	aag	cca	agc	cta	gtc	gat	gat	act	aga	579	
Asn	Asp	Lys	Gly	Thr	Asp	Phe	Lys	Pro	Ser	Leu	Val	Asp	Asp	Thr	Arg		
		175					180				185						
gga	ttg	tta	caa	ttg	tac	gaa	gct	tcg	ttt	tta	tca	gca	caa	ggc	gaa	627	
Gly	Leu	Leu	Gln	Leu	Tyr	Glu	Ala	Ser	Phe	Leu	Ser	Ala	Gln	Gly	Glu		
		190			195					200					205		
gaa	acc	cta	cat	ctt	gcc	aga	gat	ttt	gct	act	aaa	ttt	ctg	cat	aaa	675	
Glu	Thr	Leu	His	Leu	Ala	Arg	Asp	Phe	Ala	Thr	Lys	Phe	Leu	His	Lys		
				210					215					220			
aga	gta	cta	gtt	gat	aaa	gac	att	aat	ctc	tta	tca	tca	att	gaa	cgt	723	
Arg	Val	Leu	Val	Asp	Lys	Asp	Ile	Asn	Leu	Leu	Ser	Ser	Ile	Glu	Arg		
				225				230					235				
gcg	ttg	gag	ttg	cct	act	cat	tgg	agg	gtt	caa	atg	ccc	aac	gca	aga	771	
Ala	Leu	Glu	Leu	Pro	Thr	His	Trp	Arg	Val	Gln	Met	Pro	Asn	Ala	Arg		
		240					245					250					
tcc	ttc	att	gat	gct	tat	aag	agg	aga	ccc	gac	atg	aat	ccg	act	gtg	819	
Ser	Phe	Ile	Asp	Ala	Tyr	Lys	Arg	Arg	Pro	Asp	Met	Asn	Pro	Thr	Val		
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cta	gaa	cta	gct	aaa	ttg	gac	ttc	aat	atg	gtt	caa	gca	caa	ttt	caa	867	
Leu	Glu	Leu	Ala	Lys	Leu	Asp	Phe	Asn	Met	Val	Gln	Ala	Gln	Phe	Gln		
		270			275					280					285		
caa	gag	ctc	aaa	gag	gcc	tct	agg	tgg	tgg	aat	agt	acg	ggg	ctt	gtc	915	
Gln	Glu	Leu	Lys	Glu	Ala	Ser	Arg	Trp	Trp	Asn	Ser	Thr	Gly	Leu	Val		
				290				295						300			
cac	gag	ctt	ccc	ttt	gtg	aga	gat	agg	att	gtg	gaa	tgc	tac	tac	tgg	963	
His	Glu	Leu	Pro	Phe	Val	Arg	Asp	Arg	Ile	Val	Glu	Cys	Tyr	Tyr	Trp		
			305					310					315				
acg	aca	gga	gtg	gtt	gag	cgt	cgt	gaa	cat	gga	tac	gag	agg	ata	atg	1011	
Thr	Thr	Gly	Val	Val	Glu	Arg	Arg	Glu	His	Gly	Tyr	Glu	Arg	Ile	Met		
		320					325					330					
ctc	acc	aaa	ata	aat	gct	ctt	gtt	aca	aca	ata	gac	gat	gtc	ttt	gat	1059	
Leu	Thr	Lys	Ile	Asn	Ala	Leu	Val	Thr	Thr	Ile	Asp	Asp	Val	Phe	Asp		
		335				340					345						
att	tat	ggg	acg	ctt	gaa	gag	cta	caa	cta	ttc	aca	act	gct	att	caa	1107	
Ile	Tyr	Gly	Thr	Leu	Glu	Glu	Leu	Gln	Leu	Phe	Thr	Thr	Ala	Ile	Gln		
		350			355					360					365		
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Arg	Trp	Asp	Ile	Glu	Ser	Met	Lys	Gln	Leu	Pro	Pro	Tyr	Met	Gln	Ile		
				370					375					380			
tgt	tat	ctt	gct	ctc	ttc	aac	ttt	gtg	aat	gag	atg	gct	tat	gat	act	1203	

Cys	Tyr	Leu	Ala	Leu	Phe	Asn	Phe	Val	Asn	Glu	Met	Ala	Tyr	Asp	Thr		
			385					390					395				
ctt	agg	gat	aaa	ggg	ttc	aac	tcc	acc	cca	tat	cta	cga	aaa	gcg	tg	1251	
Leu	Arg	Asp	Lys	Gly	Phe	Asn	Ser	Thr	Pro	Tyr	Leu	Arg	Lys	Ala	Trp		
		400					405					410					
gtt	gat	ttg	gtt	gag	tca	tat	cta	ata	gag	gca	aag	tg	tac	tac	atg	1299	
Val	Asp	Leu	Val	Glu	Ser	Tyr	Leu	Ile	Glu	Ala	Lys	Trp	Tyr	Tyr	Met		
		415				420					425						
gga	cat	aaa	cct	agt	ttg	gaa	gaa	tat	atg	aag	aat	agt	tg	ata	tca	1347	
Gly	His	Lys	Pro	Ser	Leu	Glu	Glu	Tyr	Met	Lys	Asn	Ser	Trp	Ile	Ser		
430					435					440					445		
atc	gga	ggc	atc	ccc	att	cta	tct	cat	cta	ttt	ttc	cgg	cta	aca	gat	1395	
Ile	Gly	Gly	Ile	Pro	Ile	Leu	Ser	His	Leu	Phe	Phe	Arg	Leu	Thr	Asp		
				450					455					460			
tcg	att	gag	gaa	gag	gat	gct	gag	agt	atg	cat	aaa	tac	cat	gat	att	1443	
Ser	Ile	Glu	Glu	Glu	Asp	Ala	Glu	Ser	Met	His	Lys	Tyr	His	Asp	Ile		
			465				470						475				
gtt	cgt	gca	tcg	tgt	act	att	cta	agg	ctt	gct	gat	gat	atg	gga	aca	1491	
Val	Arg	Ala	Ser	Cys	Thr	Ile	Leu	Arg	Leu	Ala	Asp	Asp	Met	Gly	Thr		
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Ser	Leu	Asp	Glu	Val	Glu	Arg	Gly	Asp	Val	Pro	Lys	Ser	Val	Gln	Cys		
		495				500					505						
tac	atg	aat	gag	aag	aat	gct	tcg	gaa	gaa	gaa	gcg	cga	gag	cat	gtg	1587	
Tyr	Met	Asn	Glu	Lys	Asn	Ala	Ser	Glu	Glu	Glu	Ala	Arg	Glu	His	Val		
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cga	tca	ctc	ata	gac	caa	aca	tg	aag	atg	atg	aac	aag	gaa	atg	atg	1635	
Arg	Ser	Leu	Ile	Asp	Gln	Thr	Trp	Lys	Met	Met	Asn	Lys	Glu	Met	Met		
				530					535					540			
acg	tca	tca	ttt	tcc	aaa	tat	ttt	gta	caa	gtt	tct	gct	aat	ctt	gca	1683	
Thr	Ser	Ser	Phe	Ser	Lys	Tyr	Phe	Val	Gln	Val	Ser	Ala	Asn	Leu	Ala		
			545					550					555				
aga	atg	gcg	caa	tg	ata	tac	cag	cat	gaa	tct	gat	gga	ttt	ggc	atg	1731	
Arg	Met	Ala	Gln	Trp	Ile	Tyr	Gln	His	Glu	Ser	Asp	Gly	Phe	Gly	Met		
		560					565					570					
caa	cat	tca	ttg	gtg	aac	aaa	atg	ctc	aga	ggg	ttg	ttg	ttc	gac	cgc	1779	
Gln	His	Ser	Leu	Val	Asn	Lys	Met	Leu	Arg	Gly	Leu	Leu	Phe	Asp	Arg		
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Tyr	Glu																
590																	
tcacacctgat	atcaataata	attagacaaa	tggtttctgta	cgggtggccc	aaccgtcagg											1895	
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<210> 83
 <211> 591
 <212> PRT
 <213> Artificial Sequence

<400> 83
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 35 40 45
 Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro
 50 55 60
 Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser Glu Tyr Lys
 65 70 75 80
 Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala Gln Val Asn
 85 90 95
 Met Val Leu Gln Glu Glu Val Asp Ser Ile Gln Arg Leu Glu Leu Ile
 100 105 110
 Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp Arg Glu Ile
 115 120 125
 Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu Ile Asp Glu
 130 135 140
 Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr
 145 150 155 160
 Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys
 165 170 175
 Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg Gly Leu Leu
 180 185 190
 Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu Glu Thr Leu
 195 200 205
 His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys Arg Val Leu
 210 215 220
 Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg Ala Leu Glu
 225 230 235 240
 Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg Ser Phe Ile
 245 250 255
 Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val Leu Glu Leu
 260 265 270
 Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln Gln Glu Leu

275					280					285					
Lys	Glu	Ala	Ser	Arg	Trp	Trp	Asn	Ser	Thr	Gly	Leu	Val	His	Glu	Leu
290						295					300				
Pro	Phe	Val	Arg	Asp	Arg	Ile	Val	Glu	Cys	Tyr	Tyr	Trp	Thr	Thr	Gly
305					310					315					320
Val	Val	Glu	Arg	Arg	Glu	His	Gly	Tyr	Glu	Arg	Ile	Met	Leu	Thr	Lys
				325					330					335	
Ile	Asn	Ala	Leu	Val	Thr	Thr	Ile	Asp	Asp	Val	Phe	Asp	Ile	Tyr	Gly
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Thr	Leu	Glu	Glu	Leu	Gln	Leu	Phe	Thr	Thr	Ala	Ile	Gln	Arg	Trp	Asp
		355					360					365			
Ile	Glu	Ser	Met	Lys	Gln	Leu	Pro	Pro	Tyr	Met	Gln	Ile	Cys	Tyr	Leu
	370					375					380				
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385					390					395					400
Lys	Gly	Phe	Asn	Ser	Thr	Pro	Tyr	Leu	Arg	Lys	Ala	Trp	Val	Asp	Leu
				405					410					415	
Val	Glu	Ser	Tyr	Leu	Ile	Glu	Ala	Lys	Trp	Tyr	Tyr	Met	Gly	His	Lys
			420					425					430		
Pro	Ser	Leu	Glu	Glu	Tyr	Met	Lys	Asn	Ser	Trp	Ile	Ser	Ile	Gly	Gly
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Ile	Pro	Ile	Leu	Ser	His	Leu	Phe	Phe	Arg	Leu	Thr	Asp	Ser	Ile	Glu
	450					455					460				
Glu	Glu	Asp	Ala	Glu	Ser	Met	His	Lys	Tyr	His	Asp	Ile	Val	Arg	Ala
465					470					475					480
Ser	Cys	Thr	Ile	Leu	Arg	Leu	Ala	Asp	Asp	Met	Gly	Thr	Ser	Leu	Asp
				485					490					495	
Glu	Val	Glu	Arg	Gly	Asp	Val	Pro	Lys	Ser	Val	Gln	Cys	Tyr	Met	Asn
			500					505					510		
Glu	Lys	Asn	Ala	Ser	Glu	Glu	Glu	Ala	Arg	Glu	His	Val	Arg	Ser	Leu
		515					520					525			
Ile	Asp	Gln	Thr	Trp	Lys	Met	Met	Asn	Lys	Glu	Met	Met	Thr	Ser	Ser
	530					535					540				
Phe	Ser	Lys	Tyr	Phe	Val	Gln	Val	Ser	Ala	Asn	Leu	Ala	Arg	Met	Ala
545					550					555					560
Gln	Trp	Ile	Tyr	Gln	His	Glu	Ser	Asp	Gly	Phe	Gly	Met	Gln	His	Ser
				565					570					575	
Leu	Val	Asn	Lys	Met	Leu	Arg	Gly	Leu	Leu	Phe	Asp	Arg	Tyr	Glu	
			580					585					590		

<210> 84
 <211> 1967
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 computer-generated nucleic acid sequence

<220>
 <221> CDS
 <222> (13)..(1785)
 <223> computer-generated nucleic acid sequence encoding
 1,8 cineole synthase

<400> 84
 gatcaccaca ag atg tcg agt ctt ata atg caa gtt gtt att cct aag cca 51
 Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro
 1 5 10

gcc aaa att ttt cac aat aac tta ttc agc gtg att tca aaa cga cat 99
 Ala Lys Ile Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His
 15 20 25

cgt ttc agt act aca atc acc act cgt ggt ggc agg tgg gca cat tgc 147
 Arg Phe Ser Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys
 30 35 40 45

tca cta caa atg ggt aat gag atc caa act gga cga cga act gga ggc 195
 Ser Leu Gln Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly
 50 55 60

tac cag cct acc ctt tgg gat ttc agc acc att caa ttg ttc gac tct 243
 Tyr Gln Pro Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser
 65 70 75

gag tat aag gaa gag aag cac ttg atg agg gcc gca ggt atg ata gcc 291
 Glu Tyr Lys Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala
 80 85 90

caa gtg aat atg ttg ttg cag gaa gaa cta gat tcg att caa cgg ttg 339
 Gln Val Asn Met Leu Leu Gln Glu Glu Leu Asp Ser Ile Gln Arg Leu
 95 100 105

gag ttg att gat gac cta cga agg ctg ggt ata tct tgc cat ttt gac 387
 Glu Leu Ile Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp
 110 115 120 125

cgc gag atc gtt gaa ata tta aac tca aaa tat tat acc aac aat gag 435
 Arg Glu Ile Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu
 130 135 140

ata gat gaa agt gat cta tac tca aca gcc ctt aga ttc aag ctc cta 483
 Ile Asp Glu Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu
 145 150 155

aga caa tac gat ttt agc gtc tct caa gag gta ttt gat tgt ttc aag 531
 Arg Gln Tyr Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys
 160 165 170

aat gac aag ggt act gat ttc aag cca agc cta gtc gat gat act aga	579
Asn Asp Lys Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg	
175 180 185	
gga ttg tta caa ttg tac gaa gct tcg ttt tta tca gca caa ggc gaa	627
Gly Leu Leu Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu	
190 195 200 205	
gaa acc cta cat ctt gcc aga gat ttt gct act aaa ttt ctg cat aaa	675
Glu Thr Leu His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys	
210 215 220	
aga gta cta gtt gat aaa gac att aat ctc tta tca tca att gaa cgt	723
Arg Val Leu Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg	
225 230 235	
gcg ttg gag ttg cct act cat tgg agg gtt caa atg ccc aac gca aga	771
Ala Leu Glu Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg	
240 245 250	
tcc ttc att gat gct tat aag agg aga ccc gac atg aat ccg act gtg	819
Ser Phe Ile Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val	
255 260 265	
cta gaa cta gct aaa ttg gac ttc aat atg gtt caa gca caa ttt caa	867
Leu Glu Leu Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln	
270 275 280 285	
caa gag ctc aaa gag gcc tct agg tgg tgg aat agt acg ggt ctt gtc	915
Gln Glu Leu Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val	
290 295 300	
cac gag ctt ccc ttt gtg aga gat agg att gtg gaa tgc tac tac tgg	963
His Glu Leu Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp	
305 310 315	
acg aca gga gtg gtt gag cgt cgt gaa cat gga tac gag agg ata atg	1011
Thr Thr Gly Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met	
320 325 330	
ctc acc aaa ata aat gct ctt gtt aca aca ata gac gat gtc ttt gat	1059
Leu Thr Lys Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp	
335 340 345	
att tat ggt acg ctt gaa gag cta caa cta ttc aca act gct att caa	1107
Ile Tyr Gly Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln	
350 355 360 365	
aga tgg gat att gaa tca atg aag caa ctc cct cct tac atg caa ata	1155
Arg Trp Asp Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile	
370 375 380	
tgt tat ctt gct ctc ttc aac ttt gtg aat gag atg gct tat gat act	1203
Cys Tyr Leu Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr	
385 390 395	
ctt agg gat aaa ggt ttc aac tcc acc cca tat cta cga aaa gcg tgg	1251
Leu Arg Asp Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp	
400 405 410	

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gtt gat ttg gtt gag tca tat cta ata gag gca aag tgg tac tac atg 1299
Val Asp Leu Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met
415 420 425

gga cat aaa cct agt ttg gaa gaa tat atg aag aat agt tgg ata tca 1347
Gly His Lys Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser
430 435 440 445

atc gga ggc atc ccc att cta tct cat cta ttt ttc cgg cta aca gat 1395
Ile Gly Gly Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp
450 455 460

tcg att gag gaa gag gat gct gag agt atg cat aaa tac cat gat att 1443
Ser Ile Glu Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile
465 470 475

gtt cgt gca tcg tgt act att cta agg ctt gct gat gat atg gga aca 1491
Val Arg Ala Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr
480 485 490

tcg ctg gat gag gtg gag aga ggc gac gtg ccc aaa tca gtt cag tgc 1539
Ser Leu Asp Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys
495 500 505

tac atg aat gag aag aat gct tcg gaa gaa gaa gcg cga gag cat gtg 1587
Tyr Met Asn Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val
510 515 520 525

cga tca ctc ata gac caa aca tgg aag atg atg aac aag gaa atg atg 1635
Arg Ser Leu Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met
530 535 540

acg tca tca ttt tcc aaa tat ttt gta caa gtt tct gct aat ctt gca 1683
Thr Ser Ser Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala
545 550 555

aga atg gcg caa tgg ata tac cag cat gaa tct gat gga ttt ggc atg 1731
Arg Met Ala Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met
560 565 570

caa cat tca ttg gtg aac aaa atg ctc aga ggg ttg ttg ttc gac cgc 1779
Gln His Ser Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg
575 580 585

tat gag taactaatct tcgcccgggt tccaaatgaa tcaatctgtt gtgttgctgt 1835
Tyr Glu
590

tccacctgat atcaataata attagacaaa tgtttctgta cgggtggccc aaccgtcagg 1895

cccatcttcgc tcattgttcat aataaataat aaaactgtta atcaataaca aaaaaaaaaa 1955

aaaaaaaaaa aa 1967

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<210> 85
<211> 591
<212> PRT
<213> Artificial Sequence

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<400> 85
 Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro Ala Lys Ile
 1 5 10 15
 Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His Arg Phe Ser
 20 25 30
 Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys Ser Leu Gln
 35 40 45
 Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro
 50 55 60
 Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser Glu Tyr Lys
 65 70 75 80
 Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala Gln Val Asn
 85 90 95
 Met Leu Leu Gln Glu Glu Leu Asp Ser Ile Gln Arg Leu Glu Leu Ile
 100 105 110
 Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp Arg Glu Ile
 115 120 125
 Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu Ile Asp Glu
 130 135 140
 Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr
 145 150 155 160
 Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys
 165 170 175
 Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg Gly Leu Leu
 180 185 190
 Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu Glu Thr Leu
 195 200 205
 His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys Arg Val Leu
 210 215 220
 Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg Ala Leu Glu
 225 230 235 240
 Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg Ser Phe Ile
 245 250 255
 Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val Leu Glu Leu
 260 265 270
 Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln Gln Glu Leu
 275 280 285
 Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val His Glu Leu
 290 295 300
 Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp Thr Thr Gly
 305 310 315 320

Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met Leu Thr Lys
 325 330 335
 Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp Ile Tyr Gly
 340 345 350
 Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln Arg Trp Asp
 355 360 365
 Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile Cys Tyr Leu
 370 375 380
 Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr Leu Arg Asp
 385 390 395 400
 Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp Val Asp Leu
 405 410 415
 Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met Gly His Lys
 420 425 430
 Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser Ile Gly Gly
 435 440 445
 Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp Ser Ile Glu
 450 455 460
 Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile Val Arg Ala
 465 470 475 480
 Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp
 485 490 495
 Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys Tyr Met Asn
 500 505 510
 Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val Arg Ser Leu
 515 520 525
 Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met Thr Ser Ser
 530 535 540
 Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala Arg Met Ala
 545 550 555 560
 Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met Gln His Ser
 565 570 575
 Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg Tyr Glu
 580 585 590

<210> 86

<211> 1967

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

computer-generated sequence

<220>

<221> CDS

<222> (13)..(1785)

<223> computer-generated nucleic acid sequence encoding
1,8 cineole synthase

<400> 86

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gatcaccaca ag atg tcg agt ctt ata atg caa gtt gtt att cct aag cca 51
      Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro
        1             5             10

gcc aaa att ttt cac aat aac tta ttc agc gtg att tca aaa cga cat 99
Ala Lys Ile Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His
  15             20             25

cgt ttc agt act aca atc acc act cgt ggt ggc agg tgg gca cat tgc 147
Arg Phe Ser Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys
  30             35             40             45

tca cta caa atg ggt aat gag atc caa act gga cga cga act gga ggc 195
Ser Leu Gln Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly
        50             55             60

tac cag cct acc ctt tgg gat ttc agc acc att caa ttg ttc gac tct 243
Tyr Gln Pro Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser
        65             70             75

gag tat aag gaa gag aag cac ttg atg agg gcc gca ggt atg ata gcc 291
Glu Tyr Lys Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala
      80             85             90

caa gtg aat atg ttg ttg cag gaa gaa gta gat tcg ctt caa cgg ttg 339
Gln Val Asn Met Leu Leu Gln Glu Glu Val Asp Ser Leu Gln Arg Leu
      95             100             105

gag ttg att gat gac cta cga agg ctg ggt ata tct tgc cat ttt gac 387
Glu Leu Ile Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp
  110             115             120             125

cgc gag atc gtt gaa ata tta aac tca aaa tat tat acc aac aat gag 435
Arg Glu Ile Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu
        130             135             140

ata gat gaa agt gat cta tac tca aca gcc ctt aga ttc aag ctc cta 483
Ile Asp Glu Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu
        145             150             155

aga caa tac gat ttt agc gtc tct caa gag gta ttt gat tgt ttc aag 531
Arg Gln Tyr Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys
      160             165             170

aat gac aag ggt act gat ttc aag cca agc cta gtc gat gat act aga 579
Asn Asp Lys Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg
      175             180             185

gga ttg tta caa ttg tac gaa gct tcg ttt tta tca gca caa ggc gaa 627
Gly Leu Leu Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu
  190             195             200             205

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gaa acc cta cat ctt gcc aga gat ttt gct act aaa ttt ctg cat aaa	675
Glu Thr Leu His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys	
210 215 220	
aga gta cta gtt gat aaa gac att aat ctc tta tca tca att gaa cgt	723
Arg Val Leu Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg	
225 230 235	
gcg ttg gag ttg cct act cat tgg agg gtt caa atg ccc aac gca aga	771
Ala Leu Glu Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg	
240 245 250	
tcc ttc att gat gct tat aag agg aga ccc gac atg aat ccg act gtg	819
Ser Phe Ile Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val	
255 260 265	
cta gaa cta gct aaa ttg gac ttc aat atg gtt caa gca caa ttt caa	867
Leu Glu Leu Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln	
270 275 280 285	
caa gag ctc aaa gag gcc tct agg tgg tgg aat agt acg ggt ctt gtc	915
Gln Glu Leu Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val	
290 295 300	
cac gag ctt ccc ttt gtg aga gat agg att gtg gaa tgc tac tac tgg	963
His Glu Leu Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp	
305 310 315	
acg aca gga gtg gtt gag cgt cgt gaa cat gga tac gag agg ata atg	1011
Thr Thr Gly Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met	
320 325 330	
ctc acc aaa ata aat gct ctt gtt aca aca ata gac gat gtc ttt gat	1059
Leu Thr Lys Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp	
335 340 345	
att tat ggt acg ctt gaa gag cta caa cta ttc aca act gct att caa	1107
Ile Tyr Gly Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln	
350 355 360 365	
aga tgg gat att gaa tca atg aag caa ctc cct cct tac atg caa ata	1155
Arg Trp Asp Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile	
370 375 380	
tgt tat ctt gct ctc ttc aac ttt gtg aat gag atg gct tat gat act	1203
Cys Tyr Leu Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr	
385 390 395	
ctt agg gat aaa ggt ttc aac tcc acc cca tat cta cga aaa gcg tgg	1251
Leu Arg Asp Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp	
400 405 410	
gtt gat ttg gtt gag tca tat cta ata gag gca aag tgg tac tac atg	1299
Val Asp Leu Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met	
415 420 425	
gga cat aaa cct agt ttg gaa gaa tat atg aag aat agt tgg ata tca	1347
Gly His Lys Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser	
430 435 440 445	

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atc gga ggc atc ccc att cta tct cat cta ttt ttc cgg cta aca gat 1395
Ile Gly Gly Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp
450 455 460

tcg att gag gaa gag gat gct gag agt atg cat aaa tac cat gat att 1443
Ser Ile Glu Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile
465 470 475

gtt cgt gca tcg tgt act att cta agg ctt gct gat gat atg gga aca 1491
Val Arg Ala Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr
480 485 490

tcg ctg gat gag gtg gag aga ggc gac gtg ccc aaa tca gtt cag tgc 1539
Ser Leu Asp Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys
495 500 505

tac atg aat gag aag aat gct tcg gaa gaa gaa gcg cga gag cat gtg 1587
Tyr Met Asn Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val
510 515 520 525

cga tca ctc ata gac caa aca tgg aag atg atg aac aag gaa atg atg 1635
Arg Ser Leu Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met
530 535 540

acg tca tca ttt tcc aaa tat ttt gta caa gtt tct gct aat ctt gca 1683
Thr Ser Ser Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala
545 550 555

aga atg gcg caa tgg ata tac cag cat gaa tct gat gga ttt ggc atg 1731
Arg Met Ala Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met
560 565 570

caa cat tca ttg gtg aac aaa atg ctc aga ggg ttg ttg ttc gac cgc 1779
Gln His Ser Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg
575 580 585

tat gag taactaatct tcgcccgggt tccaaatgaa tcaatctgtt gtgttgctgt 1835
Tyr Glu
590

tccacctgat atcaataata attagacaaa tgtttctgta cgggtggccc aaccgtcagg 1895

cccatcttcgc tcatgttcat aataaataat aaaactgtta atcaataaca aaaaaaaaaa 1955

aaaaaaaaaa aa 1967

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<210> 87
 <211> 591
 <212> PRT
 <213> Artificial Sequence

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<400> 87
Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro Ala Lys Ile
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Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His Arg Phe Ser
          20           25           30

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Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys Ser Leu Gln
 35 40 45
 Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro
 50 55 60
 Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser Glu Tyr Lys
 65 70 75 80
 Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala Gln Val Asn
 85 90 95
 Met Leu Leu Gln Glu Glu Val Asp Ser Leu Gln Arg Leu Glu Leu Ile
 100 105 110
 Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp Arg Glu Ile
 115 120 125
 Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu Ile Asp Glu
 130 135 140
 Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr
 145 150 155 160
 Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys
 165 170 175
 Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg Gly Leu Leu
 180 185 190
 Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu Glu Thr Leu
 195 200 205
 His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys Arg Val Leu
 210 215 220
 Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg Ala Leu Glu
 225 230 235 240
 Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg Ser Phe Ile
 245 250 255
 Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val Leu Glu Leu
 260 265 270
 Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln Gln Glu Leu
 275 280 285
 Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val His Glu Leu
 290 295 300
 Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp Thr Thr Gly
 305 310 315 320
 Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met Leu Thr Lys
 325 330 335
 Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp Ile Tyr Gly
 340 345 350

Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln Arg Trp Asp
 355 360 365
 Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile Cys Tyr Leu
 370 375 380
 Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr Leu Arg Asp
 385 390 395 400
 Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp Val Asp Leu
 405 410 415
 Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met Gly His Lys
 420 425 430
 Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser Ile Gly Gly
 435 440 445
 Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp Ser Ile Glu
 450 455 460
 Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile Val Arg Ala
 465 470 475 480
 Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp
 485 490 495
 Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys Tyr Met Asn
 500 505 510
 Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val Arg Ser Leu
 515 520 525
 Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met Thr Ser Ser
 530 535 540
 Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala Arg Met Ala
 545 550 555 560
 Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met Gln His Ser
 565 570 575
 Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg Tyr Glu
 580 585 590

<210> 88

<211> 591

<212> PRT

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:
 computer-generated protein sequence

<220>

<221> VARIANT

<222> (1)..(591)

 <223> computer-generated 1,8 cineole synthase protein
 sequence variant

<400> 88

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 1 5 10 15
 Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His Arg Phe Ser
 20 25 30
 Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys Ser Leu Gln
 35 40 45
 Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro
 50 55 60
 Thr Ile Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser Glu Tyr Lys
 65 70 75 80
 Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala Gln Val Asn
 85 90 95
 Met Leu Leu Gln Glu Glu Val Asp Ser Ile Gln Arg Leu Glu Leu Ile
 100 105 110
 Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp Arg Glu Ile
 115 120 125
 Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu Ile Asp Glu
 130 135 140
 Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr
 145 150 155 160
 Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys
 165 170 175
 Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg Gly Leu Leu
 180 185 190
 Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu Glu Thr Leu
 195 200 205
 His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys Arg Val Leu
 210 215 220
 Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg Ala Leu Glu
 225 230 235 240
 Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg Ser Phe Ile
 245 250 255
 Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val Leu Glu Leu
 260 265 270
 Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln Gln Glu Leu
 275 280 285
 Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val His Glu Leu
 290 295 300
 Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp Thr Thr Gly

305	310	315	320
Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met Leu Thr Lys	325	330	335
Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp Ile Tyr Gly	340	345	350
Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln Arg Trp Asp	355	360	365
Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile Cys Tyr Leu	370	375	380
Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr Leu Arg Asp	385	390	395
Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp Val Asp Leu	405	410	415
Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met Gly His Lys	420	425	430
Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser Ile Gly Gly	435	440	445
Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp Ser Ile Glu	450	455	460
Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile Val Arg Ala	465	470	475
Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp	485	490	495
Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys Tyr Met Asn	500	505	510
Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val Arg Ser Leu	515	520	525
Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met Thr Ser Ser	530	535	540
Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala Arg Met Ala	545	550	555
Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met Gln His Ser	565	570	575
Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg Tyr Glu	580	585	590

<210> 89

<211> 591

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
computer-generated protein sequence

<220>

<221> VARIANT

<222> (1)..(591)

<223> computer-generated 1,8 cineole synthase protein
sequence variant

<400> 89

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Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro Ala Lys Ile
 1           5           10           15

Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His Arg Phe Ser
          20           25           30

Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys Ser Leu Gln
          35           40           45

Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro
          50           55           60

Thr Leu Trp Asp Phe Ser Thr Leu Gln Leu Phe Asp Ser Glu Tyr Lys
          65           70           75           80

Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala Gln Val Asn
          85           90           95

Met Leu Leu Gln Glu Glu Val Asp Ser Ile Gln Arg Leu Glu Leu Ile
          100          105          110

Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp Arg Glu Ile
          115          120          125

Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu Ile Asp Glu
          130          135          140

Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr
          145          150          155          160

Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys
          165          170          175

Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg Gly Leu Leu
          180          185          190

Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu Glu Thr Leu
          195          200          205

His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys Arg Val Leu
          210          215          220

Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg Ala Leu Glu
          225          230          235          240

Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg Ser Phe Ile
          245          250          255

Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val Leu Glu Leu
          260          265          270

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Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln Gln Glu Leu
 275 280 285
 Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val His Glu Leu
 290 295 300
 Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp Thr Thr Gly
 305 310 315 320
 Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met Leu Thr Lys
 325 330 335
 Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp Ile Tyr Gly
 340 345 350
 Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln Arg Trp Asp
 355 360 365
 Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile Cys Tyr Leu
 370 375 380
 Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr Leu Arg Asp
 385 390 395 400
 Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp Val Asp Leu
 405 410 415
 Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met Gly His Lys
 420 425 430
 Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser Ile Gly Gly
 435 440 445
 Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp Ser Ile Glu
 450 455 460
 Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile Val Arg Ala
 465 470 475 480
 Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp
 485 490 495
 Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys Tyr Met Asn
 500 505 510
 Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val Arg Ser Leu
 515 520 525
 Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met Thr Ser Ser
 530 535 540
 Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala Arg Met Ala
 545 550 555 560
 Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met Gln His Ser
 565 570 575
 Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg Tyr Glu
 580 585 590

<210> 90
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 computer-generated protein sequence

<220>
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 <222> (1)..(591)
 <223> computer-generated 1,8 cineole synthase protein
 sequence variant

<400> 90
 Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro Ala Lys Ile
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 Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His Arg Phe Ser
 20 25 30
 Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys Ser Leu Gln
 35 40 45
 Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro
 50 55 60
 Thr Leu Trp Asp Phe Ser Thr Ile Gln Val Phe Asp Ser Glu Tyr Lys
 65 70 75 80
 Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala Gln Val Asn
 85 90 95
 Met Leu Leu Gln Glu Glu Val Asp Ser Ile Gln Arg Leu Glu Leu Ile
 100 105 110
 Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp Arg Glu Ile
 115 120 125
 Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu Ile Asp Glu
 130 135 140
 Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr
 145 150 155 160
 Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys
 165 170 175
 Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg Gly Leu Leu
 180 185 190
 Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu Glu Thr Leu
 195 200 205
 His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys Arg Val Leu
 210 215 220

Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg Ala Leu Glu
 225 230 235 240
 Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg Ser Phe Ile
 245 250 255
 Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val Leu Glu Leu
 260 265 270
 Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln Gln Glu Leu
 275 280 285
 Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val His Glu Leu
 290 295 300
 Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp Thr Thr Gly
 305 310 315 320
 Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met Leu Thr Lys
 325 330 335
 Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp Ile Tyr Gly
 340 345 350
 Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln Arg Trp Asp
 355 360 365
 Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile Cys Tyr Leu
 370 375 380
 Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr Leu Arg Asp
 385 390 395 400
 Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp Val Asp Leu
 405 410 415
 Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met Gly His Lys
 420 425 430
 Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser Ile Gly Gly
 435 440 445
 Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp Ser Ile Glu
 450 455 460
 Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile Val Arg Ala
 465 470 475 480
 Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp
 485 490 495
 Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys Tyr Met Asn
 500 505 510
 Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val Arg Ser Leu
 515 520 525
 Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met Thr Ser Ser
 530 535 540

Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala Arg Met Ala
545 550 555 560

Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met Gln His Ser
565 570 575

Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg Tyr Glu
580 585 590

<210> 91

<211> 591

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
computer-generated protein sequence

<220>

<221> VARIANT

<222> (1)..(591)

<223> computer-generated 1,8 cineole synthase protein
sequence variant

<400> 91

Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro Ala Lys Ile
1 5 10 15

Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His Arg Phe Ser
20 25 30

Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys Ser Leu Gln
35 40 45

Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro
50 55 60

Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser Glu Tyr Lys
65 70 75 80

Glu Glu Lys His Val Met Arg Ala Ala Gly Met Ile Ala Gln Val Asn
85 90 95

Met Leu Leu Gln Glu Glu Val Asp Ser Ile Gln Arg Leu Glu Leu Ile
100 105 110

Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp Arg Glu Ile
115 120 125

Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu Ile Asp Glu
130 135 140

Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr
145 150 155 160

Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys
165 170 175

Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg Gly Leu Leu

180					185					190					
Gln	Leu	Tyr	Glu	Ala	Ser	Phe	Leu	Ser	Ala	Gln	Gly	Glu	Glu	Thr	Leu
	195						200					205			
His	Leu	Ala	Arg	Asp	Phe	Ala	Thr	Lys	Phe	Leu	His	Lys	Arg	Val	Leu
	210					215					220				
Val	Asp	Lys	Asp	Ile	Asn	Leu	Leu	Ser	Ser	Ile	Glu	Arg	Ala	Leu	Glu
	225					230					235				240
Leu	Pro	Thr	His	Trp	Arg	Val	Gln	Met	Pro	Asn	Ala	Arg	Ser	Phe	Ile
				245					250					255	
Asp	Ala	Tyr	Lys	Arg	Arg	Pro	Asp	Met	Asn	Pro	Thr	Val	Leu	Glu	Leu
			260					265					270		
Ala	Lys	Leu	Asp	Phe	Asn	Met	Val	Gln	Ala	Gln	Phe	Gln	Gln	Glu	Leu
		275					280					285			
Lys	Glu	Ala	Ser	Arg	Trp	Trp	Asn	Ser	Thr	Gly	Leu	Val	His	Glu	Leu
	290					295					300				
Pro	Phe	Val	Arg	Asp	Arg	Ile	Val	Glu	Cys	Tyr	Tyr	Trp	Thr	Thr	Gly
	305					310					315				320
Val	Val	Glu	Arg	Arg	Glu	His	Gly	Tyr	Glu	Arg	Ile	Met	Leu	Thr	Lys
				325					330					335	
Ile	Asn	Ala	Leu	Val	Thr	Thr	Ile	Asp	Asp	Val	Phe	Asp	Ile	Tyr	Gly
			340					345					350		
Thr	Leu	Glu	Glu	Leu	Gln	Leu	Phe	Thr	Thr	Ala	Ile	Gln	Arg	Trp	Asp
		355					360					365			
Ile	Glu	Ser	Met	Lys	Gln	Leu	Pro	Pro	Tyr	Met	Gln	Ile	Cys	Tyr	Leu
	370					375					380				
Ala	Leu	Phe	Asn	Phe	Val	Asn	Glu	Met	Ala	Tyr	Asp	Thr	Leu	Arg	Asp
	385					390					395				400
Lys	Gly	Phe	Asn	Ser	Thr	Pro	Tyr	Leu	Arg	Lys	Ala	Trp	Val	Asp	Leu
				405					410					415	
Val	Glu	Ser	Tyr	Leu	Ile	Glu	Ala	Lys	Trp	Tyr	Tyr	Met	Gly	His	Lys
			420					425					430		
Pro	Ser	Leu	Glu	Glu	Tyr	Met	Lys	Asn	Ser	Trp	Ile	Ser	Ile	Gly	Gly
		435					440					445			
Ile	Pro	Ile	Leu	Ser	His	Leu	Phe	Phe	Arg	Leu	Thr	Asp	Ser	Ile	Glu
		450				455					460				
Glu	Glu	Asp	Ala	Glu	Ser	Met	His	Lys	Tyr	His	Asp	Ile	Val	Arg	Ala
	465					470					475				480
Ser	Cys	Thr	Ile	Leu	Arg	Leu	Ala	Asp	Asp	Met	Gly	Thr	Ser	Leu	Asp
				485					490					495	
Glu	Val	Glu	Arg	Gly	Asp	Val	Pro	Lys	Ser	Val	Gln	Cys	Tyr	Met	Asn

500						505						510					
Glu	Lys	Asn	Ala	Ser		Glu	Glu	Glu	Ala	Arg	Glu	His	Val	Arg	Ser	Leu	
		515						520					525				
Ile	Asp	Gln	Thr	Trp	Lys	Met	Met	Asn	Lys	Glu	Met	Met	Thr	Ser	Ser		
	530					535						540					
Phe	Ser	Lys	Tyr	Phe	Val	Gln	Val	Ser	Ala	Asn	Leu	Ala	Arg	Met	Ala		
545					550					555					560		
Gln	Trp	Ile	Tyr	Gln	His	Glu	Ser	Asp	Gly	Phe	Gly	Met	Gln	His	Ser		
				565					570					575			
Leu	Val	Asn	Lys	Met	Leu	Arg	Gly	Leu	Leu	Phe	Asp	Arg	Tyr	Glu			
			580					585					590				

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<210> 92
<211> 591
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:
computer-generated protein sequence

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<220>
<221> VARIANT
<222> (1)..(591)
<223> computer-generated 1,8 cineole synthase protein
sequence variant
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<400> 92																	
Met	Ser	Ser	Leu	Ile	Met	Gln	Val	Val	Ile	Pro	Lys	Pro	Ala	Lys	Ile		
1				5					10					15			
Phe	His	Asn	Asn	Leu	Phe	Ser	Val	Ile	Ser	Lys	Arg	His	Arg	Phe	Ser		
			20					25					30				
Thr	Thr	Ile	Thr	Thr	Arg	Gly	Gly	Arg	Trp	Ala	His	Cys	Ser	Leu	Gln		
		35					40					45					
Met	Gly	Asn	Glu	Ile	Gln	Thr	Gly	Arg	Arg	Thr	Gly	Gly	Tyr	Gln	Pro		
	50					55					60						
Thr	Leu	Trp	Asp	Phe	Ser	Thr	Ile	Gln	Leu	Phe	Asp	Ser	Glu	Tyr	Lys		
	65				70					75					80		
Glu	Glu	Lys	His	Leu	Met	Arg	Ala	Ala	Gly	Met	Leu	Ala	Gln	Val	Asn		
				85					90					95			
Met	Leu	Leu	Gln	Glu	Glu	Val	Asp	Ser	Ile	Gln	Arg	Leu	Glu	Leu	Ile		
			100					105					110				
Asp	Asp	Leu	Arg	Arg	Leu	Gly	Ile	Ser	Cys	His	Phe	Asp	Arg	Glu	Ile		
		115					120					125					
Val	Glu	Ile	Leu	Asn	Ser	Lys	Tyr	Tyr	Thr	Asn	Asn	Glu	Ile	Asp	Glu		
	130					135					140						

Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr
 145 150 155 160
 Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys
 165 170 175
 Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg Gly Leu Leu
 180 185 190
 Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu Glu Thr Leu
 195 200 205
 His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys Arg Val Leu
 210 215 220
 Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg Ala Leu Glu
 225 230 235 240
 Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg Ser Phe Ile
 245 250 255
 Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val Leu Glu Leu
 260 265 270
 Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln Gln Glu Leu
 275 280 285
 Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val His Glu Leu
 290 295 300
 Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp Thr Thr Gly
 305 310 315 320
 Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met Leu Thr Lys
 325 330 335
 Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp Ile Tyr Gly
 340 345 350
 Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln Arg Trp Asp
 355 360 365
 Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile Cys Tyr Leu
 370 375 380
 Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr Leu Arg Asp
 385 390 395 400
 Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp Val Asp Leu
 405 410 415
 Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met Gly His Lys
 420 425 430
 Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser Ile Gly Gly
 435 440 445
 Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp Ser Ile Glu
 450 455 460

Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile Val Arg Ala
 465 470 475 480
 Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp
 485 490 495
 Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys Tyr Met Asn
 500 505 510
 Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val Arg Ser Leu
 515 520 525
 Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met Thr Ser Ser
 530 535 540
 Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala Arg Met Ala
 545 550 555 560
 Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met Gln His Ser
 565 570 575
 Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg Tyr Glu
 580 585 590

<210> 93
 <211> 591
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 computer-generated protein sequence

<220>
 <221> VARIANT
 <222> (1)..(591)
 <223> computer-generated 1,8 cineole synthase protein
 sequence variant

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 Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro Ala Lys Ile
 1 5 10 15
 Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His Arg Phe Ser
 20 25 30
 Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys Ser Leu Gln
 35 40 45
 Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro
 50 55 60
 Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser Glu Tyr Lys
 65 70 75 80
 Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala Gln Leu Asn
 85 90 95

Met Leu Leu Gln Glu Glu Val Asp Ser Ile Gln Arg Leu Glu Leu Ile
 100 105 110
 Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp Arg Glu Ile
 115 120 125
 Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu Ile Asp Glu
 130 135 140
 Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr
 145 150 155 160
 Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys
 165 170 175
 Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg Gly Leu Leu
 180 185 190
 Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu Glu Thr Leu
 195 200 205
 His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys Arg Val Leu
 210 215 220
 Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg Ala Leu Glu
 225 230 235 240
 Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg Ser Phe Ile
 245 250 255
 Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val Leu Glu Leu
 260 265 270
 Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln Gln Glu Leu
 275 280 285
 Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val His Glu Leu
 290 295 300
 Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp Thr Thr Gly
 305 310 315 320
 Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met Leu Thr Lys
 325 330 335
 Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp Ile Tyr Gly
 340 345 350
 Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln Arg Trp Asp
 355 360 365
 Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile Cys Tyr Leu
 370 375 380
 Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr Leu Arg Asp
 385 390 395 400
 Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp Val Asp Leu
 405 410 415

Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met Gly His Lys
 420 425 430

Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser Ile Gly Gly
 435 440 445

Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp Ser Ile Glu
 450 455 460

Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile Val Arg Ala
 465 470 475 480

Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp
 485 490 495

Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys Tyr Met Asn
 500 505 510

Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val Arg Ser Leu
 515 520 525

Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met Thr Ser Ser
 530 535 540

Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala Arg Met Ala
 545 550 555 560

Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met Gln His Ser
 565 570 575

Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg Tyr Glu
 580 585 590

<210> 94

<211> 591

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
computer-generated protein sequence

<220>

<221> VARIANT

<222> (1)..(591)

<223> computer-generated 1,8 cineole synthase protein
sequence

<400> 94

Met Ser Ser Leu Ile Met Gln Val Val Ile Pro Lys Pro Ala Lys Ile
 1 5 10 15Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His Arg Phe Ser
 20 25 30Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys Ser Leu Gln
 35 40 45

Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro

50					55					60					
Thr 65	Leu	Trp	Asp	Phe	Ser 70	Thr	Ile	Gln	Leu	Phe 75	Asp	Ser	Glu	Tyr	Lys 80
Glu	Glu	Lys	His	Leu 85	Met	Arg	Ala	Ala	Gly 90	Met	Ile	Ala	Gln	Val	Asn 95
Met	Val	Leu	Gln 100	Glu	Glu	Val	Asp	Ser 105	Ile	Gln	Arg	Leu	Glu	Leu	Ile 110
Asp	Asp	Leu	Arg	Arg	Leu	Gly	Ile 120	Ser	Cys	His	Phe	Asp 125	Arg	Glu	Ile
Val	Glu	Ile	Leu	Asn	Ser	Lys 135	Tyr	Tyr	Thr	Asn 140	Asn	Glu	Ile	Asp	Glu
Ser 145	Asp	Leu	Tyr	Ser	Thr 150	Ala	Leu	Arg	Phe	Lys 155	Leu	Leu	Arg	Gln	Tyr 160
Asp	Phe	Ser	Val	Ser 165	Gln	Glu	Val	Phe	Asp 170	Cys	Phe	Lys	Asn	Asp	Lys 175
Gly	Thr	Asp	Phe 180	Lys	Pro	Ser	Leu	Val 185	Asp	Asp	Thr	Arg	Gly	Leu	Leu
Gln	Leu	Tyr	Glu	Ala	Ser	Phe	Leu	Ser 200	Ala	Gln	Gly	Glu	Glu	Thr	Leu 205
His 210	Leu	Ala	Arg	Asp	Phe	Ala 215	Thr	Lys	Phe	Leu	His 220	Lys	Arg	Val	Leu
Val 225	Asp	Lys	Asp	Ile	Asn 230	Leu	Leu	Ser	Ser	Ile 235	Glu	Arg	Ala	Leu	Glu 240
Leu	Pro	Thr	His	Trp 245	Arg	Val	Gln	Met	Pro 250	Asn	Ala	Arg	Ser	Phe	Ile 255
Asp	Ala	Tyr	Lys 260	Arg	Arg	Pro	Asp	Met 265	Asn	Pro	Thr	Val	Leu	Glu	Leu 270
Ala	Lys	Leu	Asp	Phe	Asn	Met 280	Val	Gln	Ala	Gln	Phe	Gln 285	Gln	Glu	Leu
Lys 290	Glu	Ala	Ser	Arg	Trp	Trp 295	Asn	Ser	Thr	Gly	Leu	Val 300	His	Glu	Leu
Pro 305	Phe	Val	Arg	Asp	Arg 310	Ile	Val	Glu	Cys	Tyr 315	Tyr	Trp	Thr	Thr	Gly 320
Val	Val	Glu	Arg	Arg	Glu 325	His	Gly	Tyr	Glu	Arg 330	Ile	Met	Leu	Thr	Lys 335
Ile	Asn	Ala	Leu	Val	Thr	Thr	Ile	Asp 345	Asp	Val	Phe	Asp 350	Ile	Tyr	Gly
Thr 355	Leu	Glu	Glu	Leu	Gln	Leu	Phe	Thr 360	Thr	Ala	Ile	Gln 365	Arg	Trp	Asp
Ile	Glu	Ser	Met	Lys	Gln	Leu	Pro	Pro	Tyr	Met	Gln	Ile	Cys	Tyr	Leu

370	375	380
Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr Leu Arg Asp 385 390 395 400		
Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp Val Asp Leu 405 410 415		
Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met Gly His Lys 420 425 430		
Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser Ile Gly Gly 435 440 445		
Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp Ser Ile Glu 450 455 460		
Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile Val Arg Ala 465 470 475 480		
Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp 485 490 495		
Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys Tyr Met Asn 500 505 510		
Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val Arg Ser Leu 515 520 525		
Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met Thr Ser Ser 530 535 540		
Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala Arg Met Ala 545 550 555 560		
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 computer-generated protein sequence

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 <223> computer-generated 1,8 cineole synthase protein
 sequence

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 35 40 45
 Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro
 50 55 60
 Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser Glu Tyr Lys
 65 70 75 80
 Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala Gln Val Asn
 85 90 95
 Met Leu Leu Gln Gln Glu Leu Asp Ser Ile Gln Arg Leu Glu Leu Ile
 100 105 110
 Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp Arg Glu Ile
 115 120 125
 Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu Ile Asp Glu
 130 135 140
 Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr
 145 150 155 160
 Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys
 165 170 175
 Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg Gly Leu Leu
 180 185 190
 Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu Glu Thr Leu
 195 200 205
 His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys Arg Val Leu
 210 215 220
 Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg Ala Leu Glu
 225 230 235 240
 Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg Ser Phe Ile
 245 250 255
 Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val Leu Glu Leu
 260 265 270
 Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln Gln Glu Leu
 275 280 285
 Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val His Glu Leu
 290 295 300
 Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp Thr Thr Gly
 305 310 315 320
 Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met Leu Thr Lys
 325 330 335

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Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln Arg Trp Asp
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Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile Cys Tyr Leu
      370                      375                      380
Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr Leu Arg Asp
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Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp Val Asp Leu
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Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met Gly His Lys
      420                      425                      430
Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser Ile Gly Gly
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Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile Val Arg Ala
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Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp
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computer-generated protein sequence

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<223> computer-generated 1,8 cineole synthase protein
sequence

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Phe His Asn Asn Leu Phe Ser Val Ile Ser Lys Arg His Arg Phe Ser
          20           25           30

Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys Ser Leu Gln
 35           40           45

Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro
 50           55           60

Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser Glu Tyr Lys
 65           70           75           80

Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala Gln Val Asn
          85           90           95

Met Leu Leu Gln Glu Glu Val Asp Ser Leu Gln Arg Leu Glu Leu Ile
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Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp Arg Glu Ile
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Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu Ile Asp Glu
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Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr
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Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys
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Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg Gly Leu Leu
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Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu Glu Thr Leu
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His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys Arg Val Leu
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Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg Ala Leu Glu
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Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg Ser Phe Ile
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Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val Leu Glu Leu
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Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln Gln Glu Leu
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 Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp Thr Thr Gly
 305 310 315 320
 Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met Leu Thr Lys
 325 330 335
 Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp Ile Tyr Gly
 340 345 350
 Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln Arg Trp Asp
 355 360 365
 Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile Cys Tyr Leu
 370 375 380
 Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr Leu Arg Asp
 385 390 395 400
 Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp Val Asp Leu
 405 410 415
 Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met Gly His Lys
 420 425 430
 Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser Ile Gly Gly
 435 440 445
 Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp Ser Ile Glu
 450 455 460
 Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile Val Arg Ala
 465 470 475 480
 Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp
 485 490 495
 Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys Tyr Met Asn
 500 505 510
 Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val Arg Ser Leu
 515 520 525
 Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met Thr Ser Ser
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 545 550 555 560
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 1             5             10             15

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      20             25             30

Thr Thr Ile Thr Thr Arg Gly Gly Arg Trp Ala His Cys Ser Leu Gln
 35             40             45

Met Gly Asn Glu Ile Gln Thr Gly Arg Arg Thr Gly Gly Tyr Gln Pro
 50             55             60

Thr Leu Trp Asp Phe Ser Thr Ile Gln Leu Phe Asp Ser Glu Tyr Lys
 65             70             75             80

Glu Glu Lys His Leu Met Arg Ala Ala Gly Met Ile Ala Gln Val Asn
      85             90             95

Met Leu Leu Gln Glu Glu Val Asp Ser Ile Gln Arg Val Glu Leu Ile
      100            105            110

Asp Asp Leu Arg Arg Leu Gly Ile Ser Cys His Phe Asp Arg Glu Ile
      115            120            125

Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu Ile Asp Glu
      130            135            140

Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr
      145            150            155            160

Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys
      165            170            175

Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg Gly Leu Leu
      180            185            190

Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu Glu Thr Leu
      195            200            205

His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys Arg Val Leu
      210            215            220

Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg Ala Leu Glu
      225            230            235            240

Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg Ser Phe Ile

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- 211 -

				565					570					575
Leu	Val	Asn	Lys	Met	Leu	Arg	Gly	Leu	Leu	Phe	Asp	Arg	Tyr	Glu
			580					585					590	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/20120**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(6) : Please See Extra Sheet.

US CL : 435/232, 233, 252.3, 320.1, 69.1, 419; 530/350; 536/23.2, 23.6

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/232, 233, 252.3, 320.1, 69.1, 419; 530/350; 536/23.2, 23.6

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	CROTEAU, R. et al. Biosynthesis of Monoterpenes: Partial Purification, Characterization, and Mechanism of Action of 1,8-Cineole Synthase. Arch. Biochem. Biophys. 15 February 1994, Vol. 309, No. 1, pages 184-192, see the entire article, especially pages 184 & 187-192.	1, 6-8
Y	LEE, C. C. et al. Generation of cDNA Probes Directed by Amino Acid Sequence: Cloning of Urate Oxidase. Science. 11 March 1988, Vol. 239, pages 1288-1291, see the entire article.	1, 6-8



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	
A document defining the general state of the art which is not considered to be of particular relevance	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
B earlier document published on or after the international filing date	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
O document referring to an oral disclosure, use, exhibition or other means	*A* document member of the same patent family
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

05 NOVEMBER 1998

Date of mailing of the international search report

16 DEC 1998

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

TERCHAND SAIDHA

Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/20120

A. CLASSIFICATION OF SUBJECT MATTER: IPC (6):

C12N 1/20, 9/88, 9/90, 15/00; C12P 21/06; C07K 1/00; C07H 21/04

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

APS, STN Files : caplus, medline, biosis, agricola, wpids, biotechds & biosis. Search terms : bornyl diphosphate synthase, sabinene synthase, 1,8-cineole synthase, etc. Gene and protein sequence data bases searches for Specific SEQ ID NOs.